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79093

From: Portner, Ginny
Sent: Wednesday, October 30, 2002 1:58 PM
To: STIC-Biotech/ChemLib
Subject: 09/910,186
Importance: High

Please search SEQ ID Nos 9 and 10, please back translate SEQ ID NO 10. Thanks.

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Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1/1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 1/1
WWW/Internet: _____
Other (specify): _____

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnph**.

Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 13:45:26, Search time 55 seconds

922.304 Million cell updates/sec

Title: us-09-910-186a-10

Perfect score: 293

Sequence: 1 MIFPNFISYNSELKAI.....NTALLESSTHWGFPVSE 450

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

Database:

1: /SID2/gcgdata/genescp/emb1/AA1980.DAT:

2: /SID2/gcgdata/genescp/emb1/AA1981.DAT:

3: /SID2/gcgdata/genescp/emb1/AA1982.DAT:

4: /SID2/gcgdata/genescp/emb1/AA1983.DAT:

5: /SID2/gcgdata/genescp/emb1/AA1984.DAT:

6: /SID2/gcgdata/genescp/emb1/AA1985.DAT:

7: /SID2/gcgdata/genescp/emb1/AA1986.DAT:

8: /SID2/gcgdata/genescp/emb1/AA1987.DAT:

9: /SID2/gcgdata/genescp/emb1/AA1988.DAT:

10: /SID2/gcgdata/genescp/emb1/AA1989.DAT:

11: /SID2/gcgdata/genescp/emb1/AA1990.DAT:

12: /SID2/gcgdata/genescp/emb1/AA1991.DAT:

13: /SID2/gcgdata/genescp/emb1/AA1992.DAT:

14: /SID2/gcgdata/genescp/emb1/AA1993.DAT:

15: /SID2/gcgdata/genescp/emb1/AA1994.DAT:

16: /SID2/gcgdata/genescp/emb1/AA1995.DAT:

17: /SID2/gcgdata/genescp/emb1/AA1996.DAT:

18: /SID2/gcgdata/genescp/emb1/AA1997.DAT:

19: /SID2/gcgdata/genescp/emb1/AA1998.DAT:

20: /SID2/gcgdata/genescp/emb1/AA1999.DAT:

21: /SID2/gcgdata/genescp/emb1/AA2000.DAT:

22: /SID2/gcgdata/genescp/emb1/AA2001.DAT:

23: /SID2/gcgdata/genescp/emb1/AA2002.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2191	100.0	430	AA04192	Botulinum toxin hea
2	2191	100.0	430	AA04192	Botulinum toxin hea
3	2386	99.8	120	AA04514	Non-toxic modified
4	2317	96.9	462	AA06397	Clostridium botuli
5	867.5	30.3	451	AA04193	Botulinum toxin hea
6	801.5	31.5	451	AA04193	Botulinum toxin hea
7	801.5	31.5	451	AA04193	Clostridium botuli
8	588.5	24.7	449	AA04194	Botulinum toxin hea
9	588.5	24.7	449	AA04194	Botulinum toxin hea
10	588.5	24.5	837	AA07140	Native botulinum n

11	586.5	24.5	1067	21	AA073107	A mangnese supero
12	586.5	24.5	1092	21	AA073110	A mangnese supero
13	586.5	24.5	1296	27	AA055100	A mangnese supero
14	586.5	24.5	1296	27	AA055100	A mangnese supero
15	581	24.3	1095	21	AA073111	A mangnese supero
16	581	24.3	1291	19	AA068382	Clostridium botuli
17	575.5	24.2	1295	21	AA059519	Clostridium botuli
18	575.5	24.2	1295	21	AA059519	Clostridium botuli
19	576	24.1	451	19	AA068395	Clostridium botuli
20	575.5	24.1	449	21	AA073112	Botulinum toxin hea
21	575.5	24.1	449	21	AA073112	Botulinum toxin hea
22	575.5	24.1	473	19	AA068400	Botulinum toxin hea
23	573	24.0	848	22	AA04082	Clostridium botuli
24	565.5	23.6	472	19	AA068393	Clostridium botuli
25	565.5	23.6	472	19	AA068393	Clostridium botuli
26	564	23.6	1059	21	AA073109	A mangnese supero
27	564	23.6	1084	21	AA073113	A mangnese supero
28	557.5	23.3	432	31	AA077142	C. botulinum C2 tr
29	557.5	23.3	432	31	AA077142	C. botulinum C2 tr
30	557.5	23.3	437	22	AA04088	Botulinum toxin hea
31	557.5	23.3	438	19	AA068389	Clostridium botuli
32	557.5	23.3	438	19	AA068389	Clostridium botuli
33	557.5	23.3	438	21	AA077134	Synthetic botulinu
34	557.5	23.3	445	19	AA068393	Clostridium botuli
35	557.5	23.3	462	19	AA068390	Clostridium botuli
36	557.5	23.3	462	19	AA068390	Clostridium botuli
37	556.5	23.3	434	22	AA04089	Botulinum toxin hea
38	556.5	23.3	434	22	AA04089	Botulinum toxin hea
39	556.5	23.3	439	22	AA04093	Botulinum toxin hea
40	551	23.0	1032	22	AA067901	C. botulinum C2 tr
41	550	23.0	472	59	AA068394	Immunogenic type F
42	548	22.8	431	18	AA090914	Modified clostridi
43	548	22.8	431	18	AA090914	Modified clostridi
44	546	22.8	432	22	AA04096	Botulinum toxin hea
45	546	22.8	432	22	AA04096	Botulinum toxin hea

ALIGNMENTS

AA077136 standard; Protein: 430 AA.
AA077136:
AC AA077136: (first entry)
DT 08-MAY-2000
DI Synthetic botulinum neurotoxin serotype C (BoNTC) C-terminal fragment.
DE Botulinum neurotoxin, heavy chain; BoNT; serotype C;
EE C-terminal fragment; Venezuelan equine encephalitis virus replicon;
KW Vmz. botulin; vaccine; diagnosis; drug screening.
XX
OS Clostridium botulinum.
OS Synthetic.
PN W020000254.2.
XX 20-JAN-2000.
XX
PF 09-JUL-1998; 99MO-US1570.
XX
XX 10-JUL-1998; 98US-0092416.
PR 12-MAY-1999; 99US-013470.
XX
XX (USME) US MEDICAL RES INST INFECTIOUS DISEASES
PI Lee JS, Pushko P, Smith JF, Parker M, Derrbaugh MT, Smith LI
XX WPI: 2000-160827/14.
XX
XX N-PSDB: AA87214.
XX

XX	AM68397 standard; Protein; 462 kDa.	
XX	AM68397;	
XX	AM68397;	
XX	07-DEC-1998 (first entry)	
XX	Clasidium botulinum type CI toxin C fragment.	
XX	Antitoxin; vaccine; neurotoxin; toxin C; intoxication; immunogen;	
XX	botulinum; notC.	
XX	Clasidium botulinum serotype CI strain Stockholm.	
OS		

line present sequence, respectively. The amino acid sequence of the holotoxin, termed rBONT/C, in which amino acids His-229, Glu-230 and His-733 of the native sequence are substituted by Gly, Thr and Asn, respectively, i.e. the zinc binding motif (see AY08481) of the light chain holotoxin is modified, resulting in loss of endoprotease activity. DNA coding for the modified botulinum toxin (see AY2552) was assembled from 3 separate toxin fragments using

XX (OPH-.) OPHIDIAN PHARM INC.
XX
XX Thalley BS, Williams JA;
XX
XX WPI: 1998-230224.20.
XX
XX N-7508: ANV5058.
XX
XX Host cell containing recombinant expression vector encoding
XX Clostridium botulinum type B or E toxin - useful to treat humans
XX and other animals at risk of intoxication with Clostridium toxin
XX
XX
XX Example 45: Page 339-341; 428pp; English.
XX
XX This is the amino acid sequence of the histidine-tagged C fragment
XX of Clostridium botulinum (Stoccholm strain) type II neurotoxin,
XX encoded by a DNA sequence (see ANV5058) in plasmid pBR322. This
XX fragment was purified on a column of ion exchange resin (Q-Sepharose) and
XX affinity volume. The invention relates to recombinant proteins
XX containing a histidine tag and a toxin. Methods are provided which allow for the isolation of
XX soluble recombinant proteins free of significant endotoxin
XX contamination. Preferred hosts for production of recombinant
XX Clostridium botulinum type B or E toxin are used as immunogens for the production of
XX recombinant toxins are used as immunogens for the treatment of humans
XX and animals at risk of intoxication with Clostridium toxin.
XX
XX Sequence 462 AA:

Query Match 96.9%; Score 2317; DS 19; Length 452;
Best Local Similarity 59.8%; Pred. No. 28-158;
Matches 435; Conservative 1; Mismatches 0; Indels 0;

14 SILKQDINFTNINQSKTISLQNKNTLVDSYNAVERGDQVLPFPFKLGS 73
26 ALKQDINFTNINQSKTISLQNKNTLVDSYNAVERGDQVLPFPFKLGS 85
74 GEDKQYIVQNKYIVNYSMTSFSPMRINKWSLPGTIIIDSVNNGSGSIGIS 133
86 GEDKQYIVQNKYIVNYSMTSFSPMRINKWSLPGTIIIDSVNNGSGSIGIS 145
134 NFLVFTLQKQNSGINSFSDISNAPYKKNRFTVYNNQNKIYINGLIDIKV 193
146 NFLVFTLQKQNSGINSFSDISNAPYKKNRFTVYNNQNKIYINGLIDIKV 205
194 KLTQDINFTNINQSKTISLQNKNTLVDSYNAVERGDQVLPFPFKLGS 253
206 KLTQDINFTNINQSKTISLQNKNTLVDSYNAVERGDQVLPFPFKLGS 265
254 TNYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 313
314 QNTYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 325
326 TNYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 337
334 QNTYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 349
326 QNTYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 361
374 TQDQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 413
376 TQDQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 425
386 QNTYVQDQNDLQKNTYVNDLQNTYVNSQLFTFRNNQVPSKTIKRIK 437
434 SILESTINQVPSKTIKRIK 450
434 SILESTINQVPSKTIKRIK 452

RESULT 5
ANV78982 standard; Protein; 359 AA.
XX ANV78982:
XX ANV78982:

XX 20-JUN-2000 (first entry)
XX
XX C. botulinum type D toxin amino acid sequence.
XX
XX Botulinum neurotoxin type D; BoNT; botulinum; non-toxic; vaccines; poison;
XX process.
XX
XX Clostridium botulinum.
XX
XX N-7508: ANV5058-AL.
XX
XX 90320004252-AL.
XX
XX 03-FEB-2000.
XX
XX 20-JUL-1995; 9590-IB01301.
XX
XX 22-JUL-1998; 982A-004538.
XX
XX (AGRI-) AGRIC RES COUNCIL.
XX
XX De Bruyn ES, Socha AB.
XX
XX NPI: 2000-285375/18.
XX
XX N-7508: ANV5058, ANV94531.
XX
XX Non-toxic immunogenic derivative of Clostridium botulinum neurotoxin
XX type D, useful in vaccines for protection against botulinum diseases
XX and also amino acid mutation not present in the wild type D
XX neurotoxin.
XX
XX Claim 3, 4; Page 54-57; 56pp; English.
XX
XX This sequence represents the amino acid sequence of a synthetic
XX non-toxic immunogenic derivative of Clostridium botulinum toxin
XX sheep, and usually results in the death of the affected or poisoned
XX animal. The non-toxic immunogenic fragments of the C. botulinum
XX toxin (sheep type D) against BoNT type D poisoning. The non-toxic
XX fragments can be produced relatively simply and inexpensively
XX (specifically by expression on recombinant hosts). The fragments are not
XX toxic to the host and the toxicity of the fragments is reduced
XX due to the production staff is reduced.

Query Match 65.5%; Score 1595; DS 21; Length 359;
Best Local Similarity 76.0%; Pred. No. 3-2-106;
Matches 30; Conservative 33; Mismatches 56; Indels 4;
50 AVESGSDQVQLNIPFPFKLGSSEGGKVTYQNNYVNSMSEFSFKRINAW 109
1 AVESGSDQVQLNIPFPFKLGSSEGGKVTYQNNYVNSMSEFSFKRINAW 60
110 SMLQYIVDSVNGNSGIGISNFLVFTLQKQNSGINSFSDISNAPYKKNRFTV 159
61 SMLQYIVDSVNGNSGIGISNFLVFTLQKQNSGINSFSDISNAPYKKNRFTV 120
170 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 229
121 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 180
180 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 240
181 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 253
290 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 349
241 TYNNGNKKIYINGLIDIKVLTFRNNQVPSKTIKRIK 359
350 DQKVF-EDVATLQKQNSGIGISNFLVFTLQKQNSGINSFSDISNAPYKKNRFTV 407
290 FRLVFTLQKQNSGIGISNFLVFTLQKQNSGINSFSDISNAPYKKNRFTV 355

QY 408 TFFNPFSTNSLADLINEVFNFSNDSKLSQNKALVDSCTNAEVRVQDQVLA 450
DB 356 SYFSLGDDVFNHETLFIIVIKIEVWVSLSTSTHWVPFASB 399

RESULT 6
AA004093
AA004093 standard; Protein: 451 AA.
AC AA004093;

XX 11-APR-2001 (first entry)

DB Botulinum toxin heavy chain C-terminal sequence (serotype D).
XX Botulinum toxin; neurotoxin; heavy chain; recombinant expression;
XX recombinant vector; antigen; immune response; vaccine; bacterium;
XX infection.

XX Synthetic.
XX Clostridium botulinum.
XX W030067700-A2.

16-NOV-2000.

12-MAY-2000; 2000NOV-US12890.

12-MAY-1999; 9905-0138665.

12-MAY-1999; 9905-0138666.

12-MAY-1999; 9905-0138667.

12-MAY-1999; 9905-0138668.

12-MAY-1999; 9905-0138669.

12-MAY-1999; 9905-0138670.

29-JUL-1999; 9905-0146192.

(USSA) US ARMY MEDICAL RES & MATERIAL COMMAND.

Smith JA. Byrne MP. Middlebrook JL. Lapenotiere B.

WPI; 2001:015048/02.

N-7528; AA04487.

New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism

Claim 3; Fig 6b; 73pp; English.

Botulin neurotoxins are translated as a single 150 kDa polypeptide
consisting of a 100 kDa heavy chain and a 50 kDa light chain which
remain linked by a disulfide bond. Nucleic acids encoding the
heavy chain of botulinum neurotoxin (BNT) can be used in recombinant
expression vectors and expressed in transformed cells to produce
peptide antigens useful for eliciting an immune response and give
rise to a vaccine against botulism. The nucleic acids are expressible in a recombinant
organism such as Escherichia coli or Pichia pastoris. The use
of the nucleic acids in a recombinant organism to produce the
antigen is also high and cost of production is lower. The nucleic acids can
be derived from Clostridium botulinum serotypes A-G.

Sequence 451 AA:

Query Match 36.34; Score 867.5; DB 22; Length 451;
Best Local Similarity 43.24; Pred. No. 2-5e-34;
Matches 195; Conservative 84; Mismatches 145; Indels 27; Gaps 11;

2 TFFNPFSTNSLADLINEVFNFSNDSKLSQNKALVDSCTNAEVRVQDQVLA 61

DB 14 TFFNPFSTNSLADLINEVFNFSNDSKLSQNKALVDSCTNAEVRVQDQVLA 73
QY 62 PFFNPFSTNSLADLINEVFNFSNDSKLSQNKALVDSCTNAEVRVQDQVLA 120
DB 74 TFFNPFSTNSLADLINEVFNFSNDSKLSQNKALVDSCTNAEVRVQDQVLA 130
QY 121 VNNNSQNSQISLNFVFLTKLQKHQSDQNSVDSVSNAPCY-KNMFVYVNNNGSDN 179
DB 131 IQDSQSKICNENETWLDQVKNYSKLSIDPDSLSHUTGYNMFVYVNNNGSDN 190
QY 180 KYTNCKLQDTKFKVETGINSKTIPTKELNIPDGLTSDSDNMMIDYIFAKEL 239
DB 191 KYTNCKLQDTKFKVETGINSKTIPTKELNIPDGLTSDSDNMMIDYIFAKEL 242
QY 240 DQDQNLNLSQNVVQDQNSGLNYSKYNEDVLDVNNYVNSQVQVTFVRNKN 259
DB 243 SMELNIVTEQILQVNVETLQWGLKFDVTEVILNIDITAFVSNVQVQVPSB 302
QY 300 DNEGSKYIKIRKICHTQVFGDGLYQVNTNNKAYNNKEMTMA---UNISTED 356
DB 303 KYTNQSTHVSQNFVRLNDSNILLNYSKYNKTYITDQITVAGQSDQNSK 362
QY 357 IYLGAEQTDNDIMTQIQMPNMTYVTSQVFNKNGENISQICSI-GYTFPLQ 415
DB 363 VTKALQSNVQVIGV-TELSKNSVKNYQVQV-SEPR-ENMLADITKFRS --- 416
QY 416 DWYHRTLVPTQKQWASLESSTPMGFV 446
DB 417 --FNNATVAVT--NYTFKLSSTPMKFI 443

RESULT 7
AAH68398
AAH68398 standard; Protein: 451 AA.
AC AAH68398;

XX 07-DEC-1996 (first entry)

DE Clostridium botulinum type D toxin C fragment.

XX Antitoxin; vaccine; neurotoxin; toxin D; intoxication; immunogen;
KW Botulism; Botox.

XX Clostridium botulinum serotype D.

XX Synthetic.

XX Key Location/Qualifiers
XX Peptide /note= "N-terminal His tag".
XX W03008540-A1.

XX 05-MAR-1998.

XX 28-AUG-1997; 97NOV-US15394.

XX 28-AUG-1996; 96NOV-0704159.

XX (OPHT-) OPHTIDIAN PHARM INC.

XX Thayer BS, Williams JA.

XX WPI; 1998-210234/20.

XX N-PAGE; AAH20591.

XX Host cell containing recombinant expression vector encoding

Clostridium botulinum type B or E toxin - useful to treat humans

and other animals at risk of intoxication with clostridial toxin

Example 47, page 352-353, 428pp; English.

362 DTATN-----KRTIKLSSGNNPQVPMNSGVGKNTFNKN-AGNN-----IC 407
Qy 408 TYPR-----LGGDWHMYLVPFVQGVKSLSESTTH-----WFFY 446
Db 408 LQGFQATVASTY-----YTHSGHNSGKCTNFI 440

RESULT 9
LANSO094
ID AMLD4034 standard: Protein: 449 AA.
AC AABD4094:
XX
XX
11-APR-2001 (first entry)
Botulinum toxin heavy chain C-terminal sequence (serotype B).
Botulinum toxin, neurotoxin; heavy chain; recombinant expression;
recombinant vector; antigen; immune response; vaccine; bacterium;
infection.
Synthesis
Clostridium botulinum.
WQ200067100-AA2.
16-NOV-2000.
12-MAY-2000; 2000WQ-US12890.
12-MAY-1999; 99US-013365.
12-MAY-1999; 99US-013366.
12-MAY-1999; 99US-013367.
12-MAY-1999; 99US-013368.
12-MAY-1999; 99US-013369.
12-MAY-1999; 99US-013370.
12-MAY-1999; 99US-013371.
12-MAY-1999; 99US-013372.
(USSA) US ARMY MEDICAL SER & MATERIAL COMMAND.
Smith LA, Byrne WP, Middlebrook JJ, Lapointiere H;
WP: 2001-016049/02.
N-PSDB; AAN34488.

New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism
Claim 3; Fig 7b, 73p; English.

Botulin neurotoxins are translated as a single 150 kDa polypeptide
chain and then posttranslationally nicked, forming a dischain
consisting of a 100 kDa heavy chain and a 50 kDa light chain which
remain linked by a disulfide bond. Nucleic acids encoding the heavy
chain of botulinum neurotoxin (BONT) can be used in recombinant
expression vector and expressed in transformed cells to produce
peptide antigens useful for eliciting an immune response against botu-
lism. The nucleic acids are expressible in a recombinant
organism such as *Saccharicola coli* or *Pinella pastoris*. The use of
the need to culture large quantities of hazardous toxin-producing
bacteria. Production yield from the genetically engineered product
is also high and cost of production is lower. The nucleic acids can
be derived from botulinum neurotoxin serotypes A-G.

Sequence 449 AA:
Query March 24, 74; Scores 589.5; DB 23; Length 449:
Best Local Similarity 32.6%; Fred. No. 2,3e-34:

Matches	152:	Conservative	90;	Mismatches	159;	Indels	65;	Gaps
Jy	2	TTFNTNNLSNGLDILNVYVNSLQKSNKKTKTAVGSGAKVFSEHSDQLM	61					
Jy	19	SFFPLSTSLDKLLSYLNFKFKEIKLESSVLANKRVKNLVTSYSINIMNDVKR	78					
Jy	62	FPPFDKLGGSDGDGVYVAWENPVNSHTSPEHWTE---	NKGVSFLPVTI	:117		:	:	:
Jy	65	PKHPNQPG--GYNGKLTETMSIDNYLYDNKYFNKSIFSPRPMDNKIVYNNEITI	136			:	:	:
Jy	118	PTRHG--ANGSKSIQSITSELVTLKHDSKOSANESYLDSNRKP--NMFPPTVMNN	175			:	:	:
Jy	137	INCRCNMGSHVGLNHRLWLTIQDMAGIKCAATNGANSISDYTNKWFTINDOR	196			:	:	:
Jy	176	KGNMTKITNKKLIOTFYKVELZIGLNFSTKIITELMKIPDTGLITSDDSNIMWTDFVIP	215			:	:	:
Jy	197	LGSGLSKLNLNLDOKSLNKAHVINSUNILKFVNYSYIRI-----GRVPFI	243			:	:	:
Jy	236	AKEQLSDGLDLNFSOGLNVDXGMKDNLRTNFWWDLYLVNW--VANSGQIVEN	297			:	:	:
Jy	248	DREDEETELOTJLSENPNYLNKIQPMONTLOXYDEVTLNLIKAPNTDRRKDSLFIN	307			:	:	:
Jy	294	TERN---NDNPNOVGVIKRI--RNTNTRVAGSIDLPYDMINKRAFLNPMKNEMFA	349			:	:	:
Jy	350	IESTILLARALSVGIKVIOVRVNSTSDINLRKDVNTQVNIYVASKT---HLF-	361			:	:	:
Jy	368	DNISTEDIALGLRGTDQVND--NIEFGQPMMNTYYASQSFNENBSGISG	407			:	:	:
Jy	362	DIATNT-----KKTIK-SSSQRRNFMVNVSMCMKAFKNN-MGNM----	407			:	:	:
Jy	408	TYER---LGSDMVTHNLFVTGCQTALLSESTISH---ANGV	446			:	:	:
Jy	408	LIGFRQAQTVAYAST-----FTMHCHRNISMCQEPNPI	440			:	:	:
RESULT	10							
XX	AA	AK0771440						
XX	AA	AK0771440 standard; Protein: 837 AA.						
XX	AA	AKN7140:						
XX	08-MAY-2000	(first entry)						
XX	Native botulinum neurotoxin serotype A (BoNTA).							
XX	botulinum neurotoxin; heavy chain; BoCt; serotype A;							
XX	Venezuelan equine encephalitis virus replicon;							
XX	VesE; botulinus; vaccine; diagnosis; drug screening.							
XX	Clostridium botulinum.							
XX	Key Location/Qualifiers							
XX	NCBI difference 837							
XX	/note= Apparently encoded by GGTGGTGGAAGACACT G*							
XX	WP0200002524-A2.							
XX	20-JAN-2000.							
XX	09-JUL-1999; 99BK-GSI5570.							
XX	10-JUL-1999; 98US-0092416.							
XX	12-MAY-1999; 99GS-U013876.							
XX	(USME-) US MEDICAL RES INST INFECTIONS DISEASES.							
XX	Lee JS, Puekko P, Smith JT, Parker M, Dertbaugh WT, Smith L;							
XX	WPI: 2000-160827/14-							
XX	N-PUBM; ANB87216.							
XX	Novel Botulinum Neurotoxin vaccine comprising a fragment from botulinum							
XX	toxin sequences A-G, is used for inducing an immune response against							

Query Match 24.7%; Score 589.5; DB 22; Length 449;
Best Local Similarity 32.6%; Pred. No. 2.3e-34;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 7, 2002, 14:43:01, Search time 26 Seconds
(without alignments)
509,243 Million cell updates/sec

Title: us-09-910-186a-10
Perfect score: 2391
Sequence: 1 MTFPIFTVNNLSKDI.....NATSLSTSTHWFPVSE 450

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Aligned: 263574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0A
Listing first 45 summaries

Database: 1: /c9p2.6/pdata1/1/as/aa.comb.pep.*
2: /c9p2.6/pdata1/1/as/aa.comb.pep.*
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6: /c9p2.6/pdata1/1/as/aa.comb.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	586.5	24.5	1296	1	US-08-405-496A-28
2	586.5	24.5	1296	2	US-08-405-496A-28
3	586.5	24.5	1296	3	US-08-405-496A-28
4	586.5	24.5	1296	4	US-08-405-496A-28
5	586.5	24.5	1296	5	US-08-405-496A-28
6	586.5	24.5	1296	6	US-08-405-496A-28
7	586.5	24.5	1296	7	US-08-405-496A-28
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9	586.5	24.5	1296	9	US-08-405-496A-28
10	586.5	24.5	1296	10	US-08-405-496A-28
11	586.5	24.5	1296	11	US-08-405-496A-28
12	586.5	24.5	1296	12	US-08-405-496A-28
13	586.5	24.5	1296	13	US-08-405-496A-28
14	586.5	24.5	1296	14	US-08-405-496A-28
15	586.5	24.5	1296	15	US-08-405-496A-28
16	586.5	24.5	1296	16	US-08-405-496A-28
17	586.5	24.5	1296	17	US-08-405-496A-28
18	586.5	24.5	1296	18	US-08-405-496A-28
19	586.5	24.5	1296	19	US-08-405-496A-28
20	586.5	24.5	1296	20	US-08-405-496A-28
21	586.5	24.5	1296	21	US-08-405-496A-28
22	586.5	24.5	1296	22	US-08-405-496A-28
23	586.5	24.5	1296	23	US-08-405-496A-28
24	586.5	24.5	1296	24	US-08-405-496A-28
25	586.5	24.5	1296	25	US-08-405-496A-28
26	586.5	24.5	1296	26	US-08-405-496A-28
27	586.5	24.5	1296	27	US-08-405-496A-28

28	143.5	6.0	599	2	US-08-910-5518-2	Sequence 2, Appl
29	143.5	6.0	476	4	US-08-316-083-3	Sequence 3, Appl
30	143.5	6.0	335	1	US-08-231-1706-2	Sequence 1, Appl
31	143.5	6.0	216	1	US-08-180-604A-10	Sequence 10, Appl
32	143.5	6.0	216	1	US-08-180-604A-10	Sequence 10, Appl
33	138.5	5.8	286	2	US-08-405-496A-10	Sequence 10, Appl
34	138.5	5.8	286	2	US-08-405-496A-10	Sequence 10, Appl
35	138.5	5.8	286	2	US-08-405-496A-10	Sequence 10, Appl
36	138.5	5.8	286	2	US-08-405-496A-10	Sequence 10, Appl
37	128	5.4	1330	3	US-08-008-172-2	Sequence 2, Appl
38	128	5.4	1330	3	US-08-210-361-6	Sequence 6, Appl
39	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
40	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
41	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
42	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
43	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
44	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl
45	127.5	5.3	1229	3	US-08-728-470-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-480-604A-28
Patent No. 5736139
GENERAL INFORMATION: JOAN A.
APPLICANT: TRALEY, BRUCE S.
INVENTOR: TRALEY, BRUCE S.
APPLICANT: PADME, NISHA V.
INVENTOR: PADME, NISHA V.
APPLICANT: STANFORD, DOUGLAS C.
INVENTOR: STANFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND PREVENTION OF C. DIFFICILE DISEASE
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
CORRESPONDENCE ADDRESS: 220 MONTGOMERY STREET, SUITE 2200
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 08/480.604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA: US 08/405,496
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: US 08/725,154
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: US 08/161,907
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA: US 07/985,321
FILING DATE: 31-OCT-1989
ANALYST/ANALYST: ANKUR K. DIANE
REGISTRATION NUMBER: 40,027

RECEIVED/COCKET NUMBER: OHND-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELETYPE: (415) 705-8410
INFORMATION FOR SEQ ID NO. 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-405-496A-28

Query Match 24.5% Score 386.5; Db 1; Length 1296;
Best Local Similarity 31.6% Pred. No. 2.6e-39;
Matches 149; Conservative 62; Mismatches 186; Indels 55; Gaps 11;

3 IPFNFTSTNSLADLNYETNINSLKQNRKNTVQVYNSVEEDQVQNF 62
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63 IPFPD---FKLGGSGDRKIVQENIVSNWSESSFWLINWVSLP---GTT 116
909 IDNKIQFLNLS---KIVLNNAVINWNTSFLIPATYSINLWNT 163
117 IDGVNSNGSGICLVNTVPTQKQSGINWSDVSLNDQVYNNWVPTVNN 175
964 IINCNSNSWVSLGTEITLQVQKQVNTVQMTINWNTVITNR 1023
176 MNKMTYINXKILDIKVELGSGNSKFTPEIKELDTGLTSDSNTNWDYTF 235
1034 LNSKTYINSLRDLQKPIENGLINSHASINWFLDGGYOT---HRYIKYTNLF 1075
236 AKELDGDINILNSLOTVKQVNGOLYKMYKIVWVILARYMIANS----- 287
1076 DEKLENEKEITLDQSGNSGLKDFGQVDTQVPTMLADPKYVQVNVGTYW 1135
288 ---RQVENVIR-RUNNDSNGYKLIKELRGWNVTRVSGDILYFTM INKATNLPW 342
1136 LKQPSGWTYINLANSITGRTFTKNTASKONKYNKQVNVVIRVYKATL- 1193
343 KNEIYADNISTEDITVALGRDGTNDONTIPIQPMNTYITASGIFASNGEMISG 402
1194 -----ATMSAQGVKLSALEIPVGNLSGVVYVNSKEDGQITNC-KMLQJNDNGD 1246
403 ICSITGTFPLGDDGRHWVPTVQGNVSALESFST---TNGCVFVSE 150
1247 IGTGTGTFP-----NNIALVSNWNTGIDRSHLGSWEIIPVD 1289

SUBMIT 2
US-08-405-496A-28
Sequence 28, Application US/08405496A
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: CLOSTRIDIUM BOTULINUM
NUMBER OF INVENTOR: NEGOTIAT
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: ANGELO, LLP
CITY: SAN FRANCISCO
STREET: 220 MONTGOMERY STREET, SUITE 2200
STATE: CALIFORNIA
ZIP: 94104

COMPUTER READABLE FORM:
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
COPYRIGHT: 1999
APPLICATION NUMBER: US/08405496A
FILING DATE: 16-MAR-1995

CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/329,154
APPLICATION NUMBER: 08/329,154
PRIORITY DATE: 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
PRIORITY DATE: 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATMOSPHERIC INFORMATION:
NAME: ANKOLA, JANE
REGISTRATION NUMBER: 40,027
REFERENCE/COCKET NUMBER: OHND-01308
TELEPHONE: (415) 705-8410
TELETYPE: (415) 705-8410
INFORMATION FOR SEQ ID NO. 28:
SEQUENCE CHARACTERISTICS: 28:
LENGTH: 1296 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-405-496A-28

Query Match 24.5% Score 386.5; Db 2; Length 1296;
Best Local Similarity 31.6% Pred. No. 2.4e-39;
Matches 149; Conservative 82; Mismatches 186; Indels 55; Gaps 11;
OY 3 IPFNFTSTNSLADLNYETNINSLKQNRKNTVQVYNSVEEDQVQNF 62
DB 849 IPFLSVYVQQRGLSTFTKTLNITSLINAVSHLDSYKINSGVQNF 908
OY 63 IPFPD---FKLGGSGDRKIVQENIVSNWSESSFWLINWVSLP---GTT 116
DB 909 IDNKIQFLNLS---KIVLNNAVINWNTSFLIPATYSINLWNT 163
OY 117 IDGVNSNGSGICLVNTVPTQKQSGINWSDVSLNDQVYNNWVPTVNN 175
DB 964 IINCNSNSWVSLGTEITLQVQKQVNTVQMTINWNTVITNR 1023
OY 176 MNKMTYINXKILDIKVELGSGNSKFTPEIKELDTGLTSDSNTNWDYTF 235
DB 1034 LNSKTYINSLRDLQKPIENGLINSHASINWFLDGGYOT---HRYIKYTNLF 1075
OY 236 AKELDGDINILNSLOTVKQVNGOLYKMYKIVWVILARYMIANS----- 287
DB 1076 DEKLENEKEITLDQSGNSGLKDFGQVDTQVPTMLADPKYVQVNVGTYW 1135
OY 288 ---RQVENVIR-RUNNDSNGYKLIKELRGWNVTRVSGDILYFTM INKATNLPW 342
DB 1136 LKQPSGWTYINLANSITGRTFTKNTASKONKYNKQVNVVIRVYKATL- 1193
OY 343 KNEIYADNISTEDITVALGRDGTNDONTIPIQPMNTYITASGIFASNGEMISG 402
DB 1194 -----ATMSAQGVKLSALEIPVGNLSGVVYVNSKEDGQITNC-KMLQJNDNGD 1246
OY 403 ICSITGTFPLGDDGRHWVPTVQGNVSALESFST---TNGCVFVSE 450
DB 1247 IGTGTGTFP-----NNIALVSNWNTGIDRSHLGSWEIIPVD 1289

RESULT 3
Sequence 28, Application US/08405496A
Patent No. 6290940
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: CLOSTRIDIUM BOTULINUM
APPLICANT: THAYER, BRUCE S.
APPLICANT: PADHIE, NISHA V.

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MUELEN & CARROLL, LLP
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMMUNICATIONS: TELETYPE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: SPSS/PC, SPSS/MS-DOS
 CURRENT APPLICATION DATA: Patent'd Release #1.0, Version #1.30
 APPLICATION NUMBER: US/09/915.136
 CLASSIFICATION:
 PRIOR APPLICATION DATA: US 08/480,604
 FILING DATE: 04-DEC-1992
 PRIOR APPLICATION DATA: US 08/405,496
 APPLICATION NUMBER: 40,027
 PRIOR APPLICATION DATA: US 08/329,154
 APPLICATION NUMBER: 40,027
 PRIOR APPLICATION DATA: US 08/161,907
 APPLICATION NUMBER: 40,027
 FILING DATE: 07-DEC-1993
 APPLICATION NUMBER: US 07/985,321
 FILING DATE: 04-DEC-1992
 APPLICATION NUMBER: US 07/429,791
 FILING DATE: 31-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: OPHD-01763
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 397-8130
 TELEFAX: (415) 397-8138
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 438 amino acids
 TYPE: amino acid
 MODIFICATION: linear
 MOLECULE TYPE: protein

Query Match 21.34; Score 557.5; DB 4; Length 438;
 Best Local Similarity 31.44; Pred No. 1,3e-37;
 Matches 144; Conservative 80; Mismatches 180; Indels 55; Gaps 11;
 16 LQDINRYNTHNLSHLSKSWKLTDTGCVNVEYRGGDQALPTPD---FKLGS 72
 73 LSEDFRTYKTNLSINLVAHSHDUSKASINSGKWPDKQIQUNLES 129
 64 S-----KLVKNAIVNNTSVNPSFPIPTKFNLSNMETTHICMNNSSGV 118
 130 GIENLAVFLIKQDSHGS-NFSDLSNMAKY-NKHFVYTVNNGKNIYIKGLI 188
 119 SARGVLLIATDQELQKQVYKSMKEDLNKVFYTNWLNKSTIKGLI 178
 189 DTIKVGLKFNKFTFENIKFDLSLTDSDNINNKWDFYFAKELDKDQNLPL 246
 179 DQVTSLSLNTLSNMLHSDCCHT-----HYVYIKYTPDDELAKIKDVI 230
 249 NSQTYIVKTVKQVNDKNTKTYTWIDLYKRWANS-----RLGVNFR- 295
 231 DQSGNSGLACPKQVLTQDPTKMLKLPDKVYVNGVIGRWLKGSPGYSWTNI 290

294 RNNDNGNSYLLIKRIGTNTVYRGGDILYFQWLNKVALEMTKADNHSIE 355
 291 YLNSYSGTGFRIKAYSGNDINVNDRVYIVNKNKFTL-----ATNASQA 342
 356 DYALVIGLQDINNDHITLQDPNNVYIASQFNKFNISGICGTYFPLG 415
 343 GVEKLSALIEFQVNLQSYVYVVKSKMDQCTNK-KMLQDNGNSDGIQHF 397
 415 DWTNRYNVTPTVQGYASLLETS-----TRGVYVSE 450
 398 -----INLAKVVASWVNSGILSSRTLGSRMEFIVDD 431
 RESULT 7, 6-604A-75
 ; Sequence 26, Application US/08/480604
 ; Patent No. 5736139
 ; GENINFORMATION:
 ; APPLICANT: KINOR A.
 ; APPLICANT: THALLEY, BRUCE S.
 ; APPLICANT: PADRYE, NISHA V.
 ; APPLICANT: STAFFORD, DOUGLAS C.
 ; APPLICANT: STAFFORD, DOUGLAS C.
 ; TITLE OF INVENTOR: VACCINE AND ANTITOXIN FOR TREATMENT AND
 ; PREVENTION OF C. DIFFICILE DISEASE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MUELEN & CARROLL, LLP
 ; STREET: 220 MONTGOMERY STREET, SUITE 2200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; ZIP: 94104
 ; COUNTRY: UNITED STATES OF AMERICA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent'd Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/08/480,604
 ; APPLICATION NUMBER: US/08/480,604
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 624
 ; PRIOR APPLICATION DATA: US 08/422,711
 ; APPLICATION NUMBER: 40,027
 ; FILING DATE: 14-APR-1995
 ; PRIOR APPLICATION DATA: US 08/405,496
 ; APPLICATION NUMBER: 40,027
 ; FILING DATE: 15-MAR-1995
 ; PRIOR APPLICATION DATA: US 08/329,154
 ; APPLICATION NUMBER: 40,027
 ; FILING DATE: 25-OCT-1994
 ; PRIOR APPLICATION DATA: US 08/161,907
 ; APPLICATION NUMBER: 40,027
 ; FILING DATE: 07-DEC-1993
 ; PRIOR APPLICATION DATA: US 07/985,321
 ; APPLICATION NUMBER: 40,027
 ; FILING DATE: 04-DEC-1992
 ; PRIOR APPLICATION DATA: US 07/429,791
 ; APPLICATION NUMBER: 40,027
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: INGOLA, DIANE E.
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 705-8419
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 462 amino acids
 ; TYPE: amino acid
 ; MODIFICATION: linear
 ; MOLECULE TYPE: protein

[illegible][illegible]

402	IFPSIKNKLQWNOEDIVT	-----KRSKTLNDIMNIIISDFNSNITVDA	455
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[illegible]

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; SEQ ID NO 15
; LENGTH: 860

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TYPE: PPT
 ORGANISM: Clostridium tetani
 FEATURE: INFORMATION: Amino Acids 456 to 1315 of SEQ ID NO: 1
 US-08-913-880C-15

Query Match 17.8% Score 425; DB 4; Length 860;
 Best Local Similarity 26.4%; Pref. No. 2a-26;
 Matches 134; Conservative 90; Mismatches 169; Indels 114; Gaps 21;

3 1PF--NIFSTNNLSKLDINFEYNNKISLQNSKLNKLVQTSQVSNVSEGV 58

4 04 IFFSKSLQVQWNEEDIVDI-----LAKSTLLANDINDISQISFNSSVTFDA 47

5 59 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

6 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

7 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

8 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

9 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

10 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

11 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

12 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

13 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

14 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

15 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

16 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

17 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

18 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

19 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

20 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

21 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

22 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

23 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

24 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

25 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

26 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

27 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

28 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

29 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

30 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

31 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

32 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

33 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

34 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

35 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

36 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

37 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

38 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

39 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

40 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

41 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

42 111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

43 438 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

406 IFFSKSLQVQWNEEDIVDI-----LAKSTLLANDINDISQISFNSSVTFDA 459

49 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

50 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

111 NLP-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

161 PGV--NWFVFTVNNQNGNKVYIKKLDTIKVKEIYKELGNTFAGSQTIFR-DLPKDF 570

512 KLEQYVNTSISLSSKMSHLSGSGVSLGNLNLTKLQSGVQVQVTFR-DLPKDF 570

569 NATLNMWFFITNOLSSANLITNOVLMSAEITOLCA REDNNITLKLDR----- 218

571 NATLNMWFFITNOLSSANLITNOVLMSAEITOLCA REDNNITLKLDR----- 623

573 TSDSNINWFFITFAGELGROINFLNSQVTVKQWGNOLNRYETWNH-- 276

622 CANNQVYVLEDFKALPKFIEKLITSLTSLTRKQNGPLATDITFIPVAS 682

624 CANNQVYVLEDFKALPKFIEKLITSLTSLTRKQNGPLATDITFIPVAS 682

627 CANNQVYVLEDFKALPKFIEKLITSLTSLTRKQNGPLATDITFIPVAS 682

632 RGDIDFVFTNNKAY-----NFKPMNFWADNISTEDYALGLRQVTDQINKE 373

634 SKQVQLKTHDITNAPSYTNKLNITFRLN-----GLAVLIRFNNELDVP 737

638 SKQVQLKTHDITNAPSYTNKLNITFRLN-----GLAVLIRFNNELDVP 737

642 VFTYQNTASLLESTSTHCPVPSR 450

644 VFTYQNTASLLESTSTHCPVPSR 450

646 VFTYQNTASLLESTSTHCPVPSR 450

648 VFTYQNTASLLESTSTHCPVPSR 450

650 VFTYQNTASLLESTSTHCPVPSR 450

652 VFTYQNTASLLESTSTHCPVPSR 450

654 VFTYQNTASLLESTSTHCPVPSR 450

656 VFTYQNTASLLESTSTHCPVPSR 450

660 VFTYQNTASLLESTSTHCPVPSR 450

662 VFTYQNTASLLESTSTHCPVPSR 450

664 VFTYQNTASLLESTSTHCPVPSR 450

666 VFTYQNTASLLESTSTHCPVPSR 450

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692 VFTYQNTASLLESTSTHCPVPSR 450

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696 VFTYQNTASLLESTSTHCPVPSR 450

698 VFTYQNTASLLESTSTHCPVPSR 450

700 VFTYQNTASLLESTSTHCPVPSR 450

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US-08-913-880C-13

Sequence 13; Application US/0691380C

GENERAL INFORMATION:

APPLICANT: MATSUDA, Mochitomo

TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS

FILE REFERENCE: 216-380P

CURRENT APPLICATION NUMBER: US/08/913, 880C

CURRENT FILING DATE: 1997-11-24

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 13

LENGTH: 865

ORGANISM: Clostridium tetani

FEATURE:

OTHER INFORMATION: Amino Acids 451 to 1315 of SEQ ID NO: 1

US-08-913-880C-13

Query Match 17.8% Score 425; DB 4; Length 865;

Best Local Similarity 26.4%; Pref. No. 2a-26;

Matches 134; Conservative 90; Mismatches 169; Indels 114; Gaps 21;

3 1PF--NIFSTNNLSKLDINFEYNNKISLQNSKLNKLVQTSQVSNVSEGV 58

405 IFFSKSLQVQWNEEDIVDI-----LAKSTLLANDINDISQISFNSSVTFDA 462

409 QLVNFFPFKLSSE-----DRCKYVTVQNRNLYVNSMTSFSISPMIRK--WVS 110

459 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

463 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

465 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

467 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

469 QLVNFFPFKLSSE-----GTSKATLWLVNSESSEVYKAMDETNDENFNTFSLVPRKVAS 160

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US-08-913-880C-13

Sequence 13; Application US/0691380C

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Db 574 NAYLANKWYIIINERJSEANYNOWMSASBITUGAIREDNITLALDR-----626
Oy 259 TSDONINOWIETUFIKAELOKQINIFNSLOYNVYVGDOLVKNETPMRI--276
Db 617 -CHNNKXVSIHFRICFALNPKIEKLTYSITFELUPNOMLWOTVILLEVAS685
Oy 277 -----OYL---NETWANSOLVFTERRNNCFEGYKIIKKIRGNTN-UTW321
Db 686 SKDVLKNITDYMILNAPSITNGKLNHYRLYN---GLKIIERTFNELDFV740
Oy 322 BGODLIFFTMLNKAN-----NEMKXWKAADUSTEDYALGLAEOFTKQINDMI373
Db 741 ASGDIFKLYSYNNHIEVGTQDQAPNLDRLVGTNAPGIEPKMAV-----794
Oy 374 IFQJOPMNYTYASOIFKSNFENHISIGISTGYVEPLGZD-----RYERNYL423
Db 795 -----LEOLKTSVQL--KLTDOKNAS-LGLVOTNMQIONPDRILLASWY-FNHL844
Oy 424 VPTVQOQNTASLLESTFINGVFWSE450
Db 845 KUKI-----LGCWTFVPTDE960

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Arch completed: November 7, 2002, 14:47:30
 Elapsed time : 30 secs

[illegible][illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


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APPLICANT: Zsaskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travis, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, B. Howard
FILE REFERENCE: ELITRA-011A
TITLE OF INVENTION: Identification of Essential Genes in
CURRENT APPLICATION NUMBER: US/09/915.212
PRIOR APPLICATION NUMBER: 60/131,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,911
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 841
TYPE: PRT
ORGANISM: Staphylococcus aureus
Query March 5.44; Score 129; DB 10; Length 841;
Best Local Similarity 17.98; Pred. No. 0.019;
Matches 88; Conservative 81; Mismatches 160; Indels 162; Gaps 21;
6 KTFSTNSLADT
259 NLSNAQNIANGTGSTNTTTFYVDTNVRGSEVQAPAKKNAITAYKN 318
51 EYSGHQVQLNTPFPDGLSSGREGKVIYVQNEIYVNSKESISFIRNK--- 107
319 EYVLQNTISEEL-VYD---GNKAAQPLIS-STYIIN---EQLSRNATVAPKN 368
108 ---WNSLNPPTIIDVYKNSGHSI---GLISNLPVFLQAQEDSGSINFDIS 157
369 TTKQTQVTLNGLKFNPNANFKIETVDQGVDFSTFQSKLDVDTQ---FDVTS 425
158 NNAQGNKKEFVYVNNKNNKIYI---NKKL---IDTIKVA---EL 196
426 ND---NKATVVLMAQGVTSNNKQITQOVAYPDMSTNGDKIDITLDTKYTSN 481
482 SNWGSSTANGCQKTHLYDVMEDYKDGQADANEKIGVYVILGSDKELDITTD 541
246 ---ILNSLQNTVYVWVWDLNLTN 599
542 ENKQVQFQLSGNLSVESFAGTPTTANVTGDDVDSGLTDTTQIDQ---ADN 599
269 KEYVWYIDVLYNRYATNKR---QIVFNTRNN--- 299
600 SFFVTKYSLADVWSDNDGNSQSTEGKIGVGVYVNLQNGEVLGT-KTDGNGYR 659
300 -DFNGS-YKIIKIRGHT---NOTFVAGDGLDFTWTLN---KATLPMKOR 345
Db 660 DNLGSKGVYTFEPASGLTQVNTTIEDKQADGERY---DVTIIDDFQFLMG 716
346 TWANLNGSTED 356
Db 717 TSDSDSDSD 727

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RESULT 11
US-09-815-242-12751
Patent No. US2402004156841
GENERAL INFORMATION:
APPLICANT: Zsaskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travis, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, B. Howard
FILE REFERENCE: ELITRA-011A
TITLE OF INVENTION: Identification of Essential Genes in
CURRENT APPLICATION NUMBER: US/09/915.242
PRIOR APPLICATION NUMBER: 60/131,078
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-26
PRIOR FILING DATE: 2000-08-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 841
TYPE: PRT
ORGANISM: Staphylococcus aureus
Query March 5.44; Score 129; DB 10; Length 841;
Best Local Similarity 17.98; Pred. No. 0.019;
Matches 88; Conservative 81; Mismatches 160; Indels 162; Gaps 21;
6 NTFSTNSLADT
259 NLSNAQNIANGTGSTNTTTFYVDTNVRGSEVQAPAKKNAITAYKN 318
51 EYSGHQVQLNTPFPDGLSSGREGKVIYVQNEIYVNSKESISFIRNK--- 107
319 EYVLQNTISEEL-VYD---GNKAAQPLIS-STYIIN---EQLSRNATVAPKN 368
108 ---WNSLNPPTIIDVYKNSGHSI---GLISNLPVFLQAQEDSGSINFDIS 157
369 TTKQTQVTLNGLKFNPNANFKIETVDQGVDFSTFQSKLDVDTQ---FDVTS 425
158 NNAQGNKKEFVYVNNKNNKIYI---NKKL---IDTIKVA---EL 196
426 ND---NKATVVLMAQGVTSNNKQITQOVAYPDMSTNGDKIDITLDTKYTSN 481
482 SNWGSSTANGCQKTHLYDVMEDYKDGQADANEKIGVYVILGSDKELDITTD 541
246 ---ILNSLQNTVYVWVWDLNLTN 599
542 ENKQVQFQLSGNLSVESFAGTPTTANVTGDDVDSGLTDTTQIDQ---ADN 599
269 KEYVWYIDVLYNRYATNKR---QIVFNTRNN--- 299
600 SFFVTKYSLADVWSDNDGNSQSTEGKIGVGVYVNLQNGEVLGT-TKTDGNGYR 659

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333	INKEVJYFW--KNEFWJEDHUSTEDYVJALGE---	0FTQNDIN---	373
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341	SONGVNRFNKGDMGYLW--SISQALVGVWVTKTFFQDQGRQKATIDMGR	1298	
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RESULT 13
 US-10-047-676A-7
 : Application US/10047676A
 : Sequence 7
 : Filing Date 2000-07-28
 : INVENTOR INFORMATION
 : INVENTOR: JIN, JUNGIL
 : ADDRESS: 10047676A
 : GENERAL INFORMATION
 : APPLICANT: Qi Fengxia
 : APPLICANT: Confid., page W.
 : PRIORITY INFORMATION
 : PRIORITY: 03/03/03
 : TITLE OF INVENTION: MUTAGEN II BIOSYNTHESIS GENES AND PROTEINS
 : FILE REFERENCE: (JAN-17403/22
 : CURRENT APPLICATION NUMBER: US/11/047-676A
 : PRIORITY INFORMATION
 : PRIORITY: 03/03/03
 : PRIOR FILING DATE: 2000-07-28
 : NUMBER OF SEQ ID NOS: 17
 : SEQ ID NOS: 1-17
 : SEQ ID NO. PatentIn version 3.1
 : LENGTH: 990
 : TYPE: PRT
 : ORGANISM: Streptococcus mutans
 : US-10-047-676A-7

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Query Match      5.1%;  score 121.5;  DB 12;  Length 990;
Best Local Similarity 21.9%;
Matches 107;  Conservative 86;  Mismatches 170;  Indels 125;  Gaps 29;

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[illegible]

Db 711 IYLEDG 718

RESULT 14
US-08-834-665A-20
Sequence 20: Application US/0814666A
Sequence 20: Application US/0814666A
GENERAL INFORMATION:
APPLICANT: Kianthous, Harold
APPLICANT: Liseolo, Iing
APPLICANT: Yeh, Yung-Jen
APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Aam
APPLICANT: Al-Garawi, Aam
TITLE OF INVENTION: 76 KDa Helicobacter Polypeptides and
TITLE OF INVENTION: 64 corresponding Polypeptide Molecules
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Windows Version 2.0
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/834, 665A
FILING DATE: 01-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
ADDRESS: 10910186
REFERENCE/DOCKET NUMBER: 06132/038001
TELEPHONE: 617-428-0200
TELEFAX: 617-428-1043
TELEX
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULES TYPE: protein
FRAGMENT TYPE: internal
NAME/KEY: Signal Sequence
LOCATION: 1...16
OTHER INFORMATION:
US-08-834-665A-20
Query Match Similarity: 5.1%; Score 121; DB 8; Length 483;
Matches 86; Conservative 68; Mismatches 174; Indels 122; Gaps 22;

QY 193 VKELAGINSKTIITEINIKPT---GLTSSDSINSH---MIEYIFAKE-----218
Db 249 ISTLAGKDMA-IITVQLQYVSGQGLVSGSTISLSELYSEQYFTEFQGNFPR 307
QY 239 ---LQCKINILNLSQTVKWDKNDLRYKNEYVNDILNRYFANSQYVPT 254
Db 303 SVGLLNSGNGMNGVQVGLYKQPRMEFGYKAY-TITNNAIKSN---PTNS 362
QY 295 RRNNNDYKIIIRKINGNTR---VRGDDILYFQRIINNAIKNFMNWTFA 349
Db 363 ASNVFTGASGLLNLINGSDKNKYSFGITGLAALATGNSNPNKNTTNSA 422
QY 430 ---DMSTEDYVAGLRQTKCNKCNIDQY-PNNMYTFA 387
Db 432 KINTNEQFLFNTGLQ-QCHMGVGLVQIPIPTNNTYS 461
RESULT 15
US-09-815-242-2809
Sequence 5805: Application US/0915242
Sequence 5805: Application US/0915242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Zukind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Haselbeck, Robert
APPLICANT: Combs, D.
APPLICANT: Yamasaki, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes In
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELTRA-01A US-09/0915,242
SEQUENCE LENGTH: 1000 Nucleotides
CURRENT FILING DATE: 2007-03-21
PRIOR APPLICATION NUMBER: 60/131,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR FILING DATE: 2007/777
PRIOR APPLICATION NUMBER: 60/207,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
US-09-815-242-2809
Query Match Similarity: 9.3%; Score 118; DB 10; Length 993;
Matches 104; Conservative 83; Mismatches 88; Gaps 23;

QY 5 RNTSYNNLSLAKIDNEIFNINWKSILSLQNKWTL---VPSGKANSVEDQVQNP 62
Db 23 NFNLFTQYIKYSVL---QLNQKESILITFTNLCTQINFGDKVKNESLAY 80
QY 63 TB---PFFGLTSSGSEKSEKQYQYQYNNVYNWKSYSFPMILNHWNSLY-T 116
Db 81 LRMSSTPFPL-LSGIMLNLHVEYNSPTFRAYNSIQRYKVQ---GEMLYLVST 134
QY 117 ILSYNSKNSGKICISILNCTFLFKQ---NDSGSLNWSLSNANWYKNTV-T 170
Db 135 SDIETYN---LKVWNKSHINQRYINQSGSLNMLNNKQSFSSINSELLVPT 190

QY 171 VYNN--WMCNKIYNG--KLIDYKKELOIGNSKTIIFENKIPDGLTSDSONIN 226
 Db |||| :
 QY 191 VYNNUTFSLAKINDFEIMDTKVKVYTHNLSKELIYSTIIPP-----LSYSDNEN 245
 Db :
 QY 227 WARDPFI---FAKELDGDINILFNSLOTVNVKWKGNOLRN-----KEY 271
 Db :
 QY 246 YILKLSLHDDVPKEI--REIQKILAYEKET--GFCELYKDIIMHAKLFCCKY 300
 Db :
 QY 272 YVNN--IDYLSNWK-----ANSQIVFTHENNIOFNE-----CYKILK 310
 Db :
 QY 301 LQIDPKLIMINLQIDIANWISBAHLLASHNNIGFTDUKLVNRFETKFGELV 359
 Db :
 QY 311 KIRGNTNTRVGGDILYFDMINNKAVNLPMNEMTMADNETHDIAIGLREKTDIN 370
 Db :
 QY 360 KIEGHSOTGUTTFORSEEDCONI--VWAKQFJHAKRNDEY--IMKESVESLIN 415
 Db :
 QY 371 DNITFQOPMNNITYASQIKSNFNMENISGICIGTFEPFGDQWREMLVPTV--- 427
 Db :
 QY 416 DNEIHHYHAPNADVAKLYLGRFTVQVNELTVSPILASFNGATFORSHLLDTETLA 475
 Db :
 428 ---KQNY 432
 476 KLEBKSHY 484

Search completed, November 7, 2002, 14:53:54
 Job Time 24 secs


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; ZIP: 06005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; OPERATING SYSTEM: 6 WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13524
; COUNTRY: USA
; ZIP: 06005
; FILING DATE: hereavth
; CLASSIFICATION: 424
; PRIORITY: 424
; APPLICATION NUMBER: US/08/454,302
; APPLICATION NUMBER:
; FILING DATE: INFORMATION:
; NAME: Gair Massey Glacia
; REGISTRATION NUMBER: 32,257
; TELEPHONE/DOCKET NUMBER: JEFF-0154
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1154
; E-MAIL: gairmassey@aol.com
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; SEQUENCE CHARACTERISTICS: 1
; LENGTH: 1291
; TYPE: AMINO ACID
; TOPOLOGY: UNKN
; ORIGIN: 08-910-302-1
; Query Match 99.8%; Score 2386; DB 21; Length 1291;
; Best Local Similarity 100.0%; Pred. No. 3,9e-211;
; Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; 2 TIPPIFSTYNSLSLADI:NEFYFNINDEKSLONKANTLVOTSYNAVEEDVDQLN 61
; 843 TIPPIFSTYNSLSLADI:NEFYFNINDEKSLONKANTLVOTSYNAVEEDVDQLN 902
; 62 PIPDPFLGSSGDRKVTYQENKTYNMTESFSIPFIRINKWNSLPGTTITDSV 121
; 903 PIPDPFLGSSGDRKVTYQENKTYNMTESFSIPFIRINKWNSLPGTTITDSV 962
; 122 KNSNSGTSIGTSEVFLTKQESDSGISNFSYDINNAQFNKMFVTVNNMGNMKI 181
; 993 KNSNSGTSIGTSEVFLTKQESDSGISNFSYDINNAQFNKMFVTVNNMGNMKI 1022
; 182 YNSKLIDITIKVKELG:G:INFSKT:TFPIK:PTGGLT:SDSNI:NMK:RPT:IFAKELG 241
; 1023 YNSKLIDITIKVKELG:G:INFSKT:TFPIK:PTGGLT:SDSNI:NMK:RPT:IFAKELG 1092
; 242 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 301
; 1083 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 1142
; 302 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 361
; 1143 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 1202
; 362 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 421
; 1203 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 1262
; 422 YLVPVQKQASLLESTINGFPVSE 450
; 1263 YLVPVQKQASLLESTINGFPVSE 1291
; 242 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 301
; 1083 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 1142
; 302 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 361
; 1143 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 1202
; 362 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 421
; 1203 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 1262
; 422 YLVPVQKQASLLESTINGFPVSE 450
; 1263 YLVPVQKQASLLESTINGFPVSE 1291
; RESULT 6
; US-08-453-186A
; Sequence 1354; Application US/03791537
; GENERAL INFORMATION:
; APPLICANT: Biocor, Inc.
; APPLICANT: Dazner, Joseph
; APPLICANT: Dazner, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

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; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 361/10
; CURRENT APPLICATION NUMBER: US/08/791-537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13524
; COUNTRY: USA
; ZIP: 06005
; FILING DATE: hereavth
; CLASSIFICATION: 424
; PRIORITY: 424
; APPLICATION NUMBER: US-08/791-537,13524
; APPLICATION NUMBER:
; FILING DATE: INFORMATION:
; NAME: Gair Massey Glacia
; REGISTRATION NUMBER: 32,257
; TELEPHONE/DOCKET NUMBER: JEFF-0154
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1154
; E-MAIL: gairmassey@aol.com
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; SEQUENCE CHARACTERISTICS: 1
; LENGTH: 1291
; TYPE: AMINO ACID
; TOPOLOGY: UNKN
; ORIGIN: 08-791-537-13524
; Query Match 99.8%; Score 2386; DB 21; Length 1291;
; Best Local Similarity 100.0%; Pred. No. 3,9e-211;
; Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; 2 TIPPIFSTYNSLSLADI:NEFYFNINDEKSLONKANTLVOTSYNAVEEDVDQLN 61
; 843 TIPPIFSTYNSLSLADI:NEFYFNINDEKSLONKANTLVOTSYNAVEEDVDQLN 902
; 62 PIPDPFLGSSGDRKVTYQENKTYNMTESFSIPFIRINKWNSLPGTTITDSV 121
; 903 PIPDPFLGSSGDRKVTYQENKTYNMTESFSIPFIRINKWNSLPGTTITDSV 962
; 122 KNSNSGTSIGTSEVFLTKQESDSGISNFSYDINNAQFNKMFVTVNNMGNMKI 181
; 993 KNSNSGTSIGTSEVFLTKQESDSGISNFSYDINNAQFNKMFVTVNNMGNMKI 1022
; 182 YNSKLIDITIKVKELG:G:INFSKT:TFPIK:PTGGLT:SDSNI:NMK:RPT:IFAKELG 241
; 1023 YNSKLIDITIKVKELG:G:INFSKT:TFPIK:PTGGLT:SDSNI:NMK:RPT:IFAKELG 1092
; 242 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 301
; 1083 KDTNLSNLOTVYVWQWQNDLRYKNEYMTWNTDLYNFWANSRLQVTFRRNNDF 1142
; 302 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 361
; 1143 NSGKYLIIKRIKNGTAVAGGDILYFDQKINNAKLFNMEWTADNISTEDYALIG 1202
; 362 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 421
; 1203 LERQTKDNINFIQOPNNHTYTFASQIFKSNNGENISGICSTGYRFLGSDWTHN 1262
; 422 YLVPVQKQASLLESTINGFPVSE 450
; 1263 YLVPVQKQASLLESTINGFPVSE 1291
; RESULT 7
; US-08-791-537-9505
; Sequence 9055; Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocor, Inc.
; APPLICANT: Dazner, Joseph
; APPLICANT: Dazner, Joseph
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 361/210
; CURRENT APPLICATION NUMBER: US/08/791-537
; CURRENT FILING DATE: 2001-02-22
; SOFTWARE: Patent in version 3.0
; SEQ ID NOS: 151055
; LENGTH: 1291
; TYPE: PRT
; TOPOLOGY: UNKN
; ORIGIN: 08-791-537-9505
; Query Match 99.8%; Score 2386; DB 21; Length 1291;
; Best Local Similarity 100.0%; Pred. No. 3,9e-211;
; Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

422 YLVPVKVGNASLESTHCPVPSVE 1390
1257 YLVPVKVGNASLESTHCPVPSVE 1395

PCUS9711
PCUS9711394 65
1 PCUS9711394 65 Application PC/TUS9711394
1 GENERAL INFORMATION:
1 APPLICANT: Williams, James A.
1 TITLE OF INVENTION: Multivalent Vaccine For Clostridium
1 TITLE OF INVENTION: Botulinum Neurotoxin
1 NUMBER OF SOURCES: 82
1 ADDRESS: 220 Montgomery Street, Suite 2200
1 ADDRESS: Medlan & Carroll
1 CITY: San Francisco
1 STATE: California
1 COUNTRY: United States of America
1 ZIP: 94104
1 MEDIUM TYPE: Flexible Copy.
1 COMPUTER: IM PC compatible
1 SOFTWARE: PC/US9711394 65
1 CURRENT APPLICATION DATA:
1 APPLICATION NUMBER: PC/TUS9711394
1 CLASSIFICATION:
1 ATTORNEY/AGENT INFORMATION:
1 NAME: Eschen, Lane
1 REGISTRATION NUMBER: 40-027
1 REFERENCE/DOCKET NUMBER: OPID-02304
1 TELECOMMUNICATION INFORMATION:
1 TELEPHONE: (415) 397-8338
1 TELEFAX: (415) 397-8338
1 INFORMATION FOR SEQ ID NO: 62:
1 SEQUENCE CHARACTERISTICS
1 TYPE: amino acids
1 TOPOLOGY: linear
1 MOLECULE: protein
1 (MSU) 1394-65

2	TIPNTPYVNSLKDIDNFTFNPNISKILSLOHKKKTLDTSCYANYSKDYOVAN	61
47	TIPNTPYVNSLKDIDNFTFNPNISKILSLOHKKKTLDTSCYANYSKDYOVAN	106
63	TIPNTPYVNSLKDIDNFTFNPNISKILSLOHKKKTLDTSCYANYSKDYOVAN	121
84	PITPTPTGLSSGDRCKVTQNMENYNKSNVSPESIPKSLNNVSNPTIDSLN	136
90	PITPTPTGLSSGDRCKVTQNMENYNKSNVSPESIPKSLNNVSNPTIDSLN	161
122	NNKSNNGSICITSNFTPLTKONSGESQISINYSNNAPKTFYFVNNNGMKI	181
197	NNKSNNGSICITSNFTPLTKONSGESQISINYSNNAPKTFYFVNNNGMKI	226
182	TNKKGLDITKVKELTQKSNITFENIPGGLITQSSNNINISGVIFAKGLD	104
107	TNKKGLDITKVKELTQKSNITFENIPGGLITQSSNNINISGVIFAKGLD	1086
242	KDNILNLSLTQVNVWDKGLNKKYKMTWIDILKRYKASGSLVFNRRNDF	301
108	KDNILNLSLTQVNVWDKGLNKKYKMTWIDILKRYKASGSLVFNRRNDF	1146
302	HEKTLIKITIKNGVNTDVGGLIYDFQINNKATIKPKENETKADMSITDTG	361
1147	HEKTLIKITIKNGVNTDVGGLIYDFQINNKATIKPKENETKADMSITDTG	1206
362	HEKTLIKITIKNGVNTDVGGLIYDFQINNKATIKPKENETKADMSITDTG	421
1207	HEKTLIKITIKNGVNTDVGGLIYDFQINNKATIKPKENETKADMSITDTG	1266

[illegible]

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OY 374 IFOIQPHNNYTYASQIFKSNFNGENISGICSTGYRFLGDMGMYRNTLVPTVQOYTA 433
DB 386 IFOQPHNNYTYASQIFKSNFNGENISGICSTGYRFLGDMGMYRNTLVPTVQOYTA 445
OY 434 ILESSTSTHNGFVPSV 450
DB 446 ILESSTSTHNGFVPSV 462

RESULT 12 159-62
; Sequence 62, Application US/08704159
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; TITLE OF INVENTION: Multivalent Vaccine For Clostridium
; TITLE OF INVENTION: Botulinum Neurotoxin
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll
; STREET: 3750 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible-PC
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/704,159
; CLASSIFICATION: 424
; NAME/AGENT INFORMATION:
; REGISTRATION NUMBER: 45,027
; REFERENCE/DOCKET NUMBER: OPED-02304
; TELEPHONE: (415) 705-8310
; TELEFAX: (415) 397-8338
; INFORMATION: SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; 08-704-159-62
; Query Match: 96.94; Score 2317; Db 11; Length 462:
; Best Local Similarity 99.84; Pred. No. 2,1e-205;
; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 14 SLKLDINFTNFNNHCKSLQNKRLVDTSTNAYVSESDVOLNFPFPPFKLSS 73
DB 26 ALLKIDINFTNFNNHCKSLQNKRLVDTSTNAYVSESDVOLNFPFPPFKLSS 85
OY 74 GEDKGVITQVNNYVNNYSKESFISFWIRKNNWSNLPOTTIDSVNNNSGIGIS 133
DB 86 GEDKGVITQVNNYVNNYSKESFISFWIRKNNWSNLPOTTIDSVNNNSGIGIS 145
OY 134 NPLVFTLKNSGSGEINFSIDSNNAQGNKNNFVYVNNKNNKNTIKSLDITRY 193
DB 146 NPLVFTLKNSGSGEINFSIDSNNAQGNKNNFVYVNNKNNKNTIKSLDITRY 205
OY 194 KLTGIDGNKATITEINPTGLTIDSDSNINMKIHPITFAELQDQNDLNFNSQY 253
DB 206 KLTGIDGNKATITEINPTGLTIDSDSNINMKIHPITFAELQDQNDLNFNSQY 265
OY 254 THVYDQWDLNLTNRYTWNIDYJMYTANSQYVPTNRNNRNNFEDKIKIKIKR 313
DB 266 THVYDQWDLNLTNRYTWNIDYJMYTANSQYVPTNRNNRNNFEDKIKIKIKR 325

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OY 314 GNTVTVRPGDILYDWTINNNKYNLPMNKNWAGNHSIEDTVALGSRQKDNONI 373
DB 376 GNTVTVRPGDILYDWTINNNKYNLPMNKNWAGNHSIEDTVALGSRQKDNONI 385
OY 374 IFOIQPHNNYTYASQIFKSNFNGENISGICSTGYRFLGDMGMYRNTLVPTVQOYTA 433
DB 386 IFOQPHNNYTYASQIFKSNFNGENISGICSTGYRFLGDMGMYRNTLVPTVQOYTA 445
OY 434 ILESSTSTHNGFVPSV 450
DB 446 ILESSTSTHNGFVPSV 462

RESULT 13
; Sequence 62, Application US/10271012
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; TITLE OF INVENTION: Multivalent Vaccine For Clostridium
; TITLE OF INVENTION: Botulinum Neurotoxin
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll
; STREET: 3750 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible-PC
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/10/271,012
; CLASSIFICATION: <unknown>
; NAME/AGENT INFORMATION:
; REGISTRATION NUMBER: 45,027
; REFERENCE/DOCKET NUMBER: OPED-02304
; TELEPHONE: (415) 705-8310
; TELEFAX: (415) 397-8338
; INFORMATION: SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; 10-271-012-62
; Query Match: 96.94; Score 2317; Db 26; Length 462:
; Best Local Similarity 99.84; Pred. No. 2,1e-205;
; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 14 SLKLDINFTNFNNHCKSLQNKRLVDTSTNAYVSESDVOLNFPFPPFKLSS 73
DB 26 ALLKIDINFTNFNNHCKSLQNKRLVDTSTNAYVSESDVOLNFPFPPFKLSS 85
OY 74 GEDKGVITQVNNYVNNYSKESFISFWIRKNNWSNLPOTTIDSVNNNSGIGIS 133
DB 86 GEDKGVITQVNNYVNNYSKESFISFWIRKNNWSNLPOTTIDSVNNNSGIGIS 145
OY 134 NPLVFTLKNSGSGEINFSIDSNNAQGNKNNFVYVNNKNNKNTIKSLDITRY 193
DB 146 NPLVFTLKNSGSGEINFSIDSNNAQGNKNNFVYVNNKNNKNTIKSLDITRY 205

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Dd 623 NYTMDIFGKFLAKDIAKRNII...NULDMT...-EFKNQDL 661
 Qy 327 LYTMSTNNKAKNFKMKNSTNNKST...-EDYALGLE- 364
 Dd 662 LYTMSEKRNKSL...-NIIINNNKSTSLRSEIPNENDEHILCLDYLGINNR 718
 Qy 345 -OTQDHWITRIGOP...-NNVNTYAGDSNPNKRN 400
 Dd 719 LLQANNKNSVMOVKRYEVDPLNENKYPILF-NLKGSH 763
 RESULT 2
 US-10-092-411A-3716
 ; GENERAL INFORMATION :
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: 032796-101
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US/09/134,001
 ; PRIOR FILING DATE: 1997-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-08-14
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; SEQ ID NO 3716
 ; LENGTH: 1325
 ; ORGANISM: Staphylococcus epidermidis
 Query Match 5.1k; Score 121.5; DB 6; Length 1335;
 Best Local Similarity 19.8k; Pred No. 0.46;
 Matches 97; Conservative 74; Mismatches 193; Indels 127; Gaps 23;
 OY 10 TYNLALQDITNFKYFNINQKSLISLQNKNTLVDSOTNAEVEEDQV 69
 900 TANNP...-IMRGDGNATVLLQDSNTPL...-QMNNDVDTN - 942
 70 LGSSGDEGKIVTNNKNSVNSM...-SFSISPIRNKNSLNP 114
 943 IGGDQYIGKATYEPFNILSVIATHTQKQALPANTLANQANNAKNAVYK -D 996
 115 VITQDSVNNKNSNGIGIENFVATQNESINFSID-LSNAPYNAFVTVN 173
 997 LYLTQYNNQTN...-IAGLII...-QNSDAPSTFTNTYNNKSY -THEPTK 1046
 174 NMGKMKYINSLKIDITKVELQLN...-SKTTFENKIDPGLIT 219
 1047 ARNYSVPEYV-PTFTIIONINYNWYQQLDQKYNKSDVLEKATYATL 1105
 220 SSSDNN...-MIRDPYIFAKELDQKIDIFEN-LSQYTVNVDYWN 263
 1106 NNAULGSLKTPQVONPLANSNYSQIK-NAMDTNRLNSLKY...-Q 1154
 264 DAKRYNTVYDILNRYN...-YANSRPIVTFNRNNPDSNYIIKRIK-GNND 318
 1125 FLRDPQNT-BAQALNKLKCKVLENGAATSOAKRYNETLISHALVTGNTS 1213
 QY 319 TRVRSKRL...-TFMTNNKNNKNNKNNKNNKNNSTEDYALGLEKTYDNNKIFQ 376
 Dd 124 CLARGVNSKQYTGKRYNNVFQIA...-PDNALVDGKRYKAMGNTSVSKALG 1270
 QY 377 TPONNNTYVAGS...-IFENNGENTSGTICSTYFRLQDQYNNB...- 421
 Dd 121 ARFENISVAGQNTVETERNP...-POTHGATDINWYNAQVLYQTKDKE 1324
 QY 422 ----LYPTK 428
 Dd 1325 VKRYEPTK 1335

RESULT 3
 US-10-092-411A-5314
 ; GENERAL INFORMATION :
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: 032796-101
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 69/134,001
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; SEQ ID NO 5314
 ; LENGTH: 1330
 ; ORGANISM: Staphylococcus epidermidis
 Query Match 5.0k; Score 119.5; DB 6; Length 930;
 Best Local Similarity 21.0k; Pred No. 0.39;
 Matches 98; Conservative 63; Mismatches 184; Indels 121; Gaps 23;
 OY 9 STYN...-NBLKADITNFKYFNINQKSLISLQNKNTLVDSOTNAEVEEDQV 59
 Dd 224 STYNDKISNKGRLANFZINENVPVLSLTSQASQKVVY...-NLKADGNNY 278
 OY 60 LNFIPFDKLGSSGDEGKIVTNNKNSVNSM...-FYFTKQNDQESINFSIDNNKPNKNNP 118
 Dd 279 NULKVTQOSTBQDSGGLKAMANDLIVDTF...-NNK...-VD 317
 OY 119 DVYNNNSGWSIGLSH...-NKLIDITNFKYKGLKNSFTSEINLE -TGLI 218
 Dd 318 DVKSDQYVNDKATVYLSOLDSFAIPKIN-SRLIANGDITNKOITTYD 376
 OY 170 TYNWNGKNT...-T...-NKLIDITNFKYKGLKNSFTSEINLE -TGLI 218
 Dd 377 DYENIKALKATSYDCKSPNNKTKDVEKTALESN-KTTFYQPNENRANL 434
 OY 219 TSESDIN...-MIRDPYIFAKELDQKIDIFEN-LSQYTVNVDYWN 263
 Dd 435 QMNTDITNRYTVETITVITVAPYAK...-TNNISONGDEGSLID -SIIKYK 489
 OY 270 TWANSDQYVTFNRNNPDSNYIIKRIKINQNDVRSQDGI- 326
 Dd 430 VQDNKNNKNSIGTICSTYFRLQDQYNNB...-THDQY...-LNNNDVNFQNS 534
 OY 327 LYFDMT...-NNKAYNFKMKNKMEAD-NSTEDYALGLEKTYDNNKIFQ - 378
 Dd 535 PIILKYSDNPMDQDITQGYVYVATVITNGER...-KASTDINFTSSG 587
 OY 379...-PHANTYVAGS...-IFENNGENTSGTICSTYFRLQDQYNNB...- 421
 Dd 588 QQQDGLPDKTKIGYVWDYDQGLGNTNANRFLSNVLYLTL 693

RESULT 4
 US-10-092-411A-4675
 ; GENERAL INFORMATION :
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: 032796-101
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US/09/134,001

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PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5676
SEQ ID NO: 4675
SEQUENCE:
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-092-411A-4675

Query Match
Best Local Similarity 4.94; Score 116; DB 6; Length 691;
Matches 116; Conservative 84; Mismatches 176; Indels 224; Gaps 33;

1 MTPTNFIISVYVNS---LACINIEFNINISKIL--- 33
5 MSIPNG--VTSNINAECTQGRTHKVEVLEIITDITGFNNGNNGNANFNKFP 62
34 --SLGN--RNTL--VTGTYNNE--VEE-----GDQVNPITFPD 67
63 QGELNHYKRNKVFRISSNLNENFKYELFLVLVDSGSLNLTAVKLNKAF-- 121
68 FLUGSSGRKRVYQVNNENIVNSNFSISFPHN---NW--SNP--G 114
122 -----FNVSINISLLOD--VLEKHPNLTNPKTIPKRS 159
136 YTTIISVNSMSGICITSNLTFTYFKONSDRSISVDSLH--NAPNHWVTV 171
160 STIVGVYKSLAPKAPNINLTKIKRHEKEDNDKRLKGLYK---TL 215
172 TUNSGNHWYVINKLIDITKVELTQVTSKFIITFIKIDITDGLTISGDNINMHD 231
216 TGN-----VLPSEIISIMELA-----KYLEKRLITGD--IAPAT 253
232 FYI-----PAELEDGILNLSLO-----YTVKVDWGH--CLVKNYETWY 278
254 FYIVLIRFNTSNKRTSNKSNELSDCHIAV--TEFLPAANKHLOSTINVREZLT 313
276 LNRWV-----VANSPLVFT-----NTRNNNDNFETKILIKRGNND-- 318
314 IRFPLMODITQNALPQDREYTPQCPREKKNSSQDYTPVLEQLPHEINOLH 373
319 -----TVRGSDILYDFMTINNA-----YNL-----PKNMTWADNS 352
374 KOLPWNVAKYGLDGLV-----HLONCLAKNKNISITIDATFVGWGRIFD 428
353 STEDYALGLAE--OFKCN--DNITQI--QPNNTYVYASQAFKSNEN---GENT-- 400
425 KLADINLVANSKSTSENFNFNITLTKIKRHEKEDNDKRLKGLYKNTID 488
401 --STICSDITRFLGGDWHNNTVPTVQG-----NATSLIEST 439
488 EGEELHETKTPQ-----BETAVKLNGADULLIGELANSPEMLTKALIDOT 541

RESULT 5
US-10-092-411A-3242
Sequence 3242, Application US/10092411A
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTOR: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: 05010-00000
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/052, 411A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 5676
SEQUENCE:
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-092-411A-3242

Query Match
Best Local Similarity 4.94; Score 116.5; DB 6; Length 151;
Matches 97; Conservative 90; Mismatches 175; Indels 181; Gaps 27;

1 NUMBERS OF SEQ ID NOS: 5676
2 SEQ ID NO 3242
3 LENGTH: 151
4 ORGANISM: Staphylococcus epidermidis
5 US-10-092-411A-3242

Query Match
Best Local Similarity 17.94; Pred. No. 0.81;
Matches 97; Conservative 90; Mismatches 175; Indels 181; Gaps 27;

3 IPIFYSINSLKADINIEFNINISKILSNKNTLV---DTSYVNWSEGDV 58
72 LSSPPTSTNATVNAVKA---DEILANVOOYVTKTAKTGVNQRVNS 125
59 QLNP-ITPFD--FKLSSGSDKGV-----VTQN---ENIVNSMTSFS 100
126 EIN--PSSNGLAPPTQPVGVNVAHGSQSDPTNLTLPVGVNVAHNP 183
101 FRIKNNKSLAGSTYIDV-----KNSGSDI----- 131
184 PKRINE--VGIITFTVINDHNEEITFETSKRSVTKKQKILQOTVYVQ 241
137 -----INTVFTYFKONSDRSISVDSLH--NAPNHWVTV 171
372 PCKEILNATVNAVKAHSEEDVYVNTQITDQ-----VITNSG 287
85 GLIDITKVELTQVTSKFIITFIKIDITDGLTISGDNINMHD 231
288 SLIDQVNE--EQTFAVLOQQQ---EVSAGALV---LNVKVNANSQV 294
321 SNLFTYKQR--KIDLDNATVNDHSLNLTESMATFVQGP----- 371
294 RNNKNSNRYKILITRIGTQNTVPTVQG-----DILVETMINKAYLN 345
372 KKKKEED-----FRLNATQVQRVQVQLRDEMGSLTRFNHAKNKL 425
346 -----TWANISFEDYALIGREQ--KIDNIDITQVQPNNTYVYASQ 394
426 EDVWVLSLQVQTSINVTYVTSFVDEYKALKIKKEST-----LFE 475
395 PENSISGSCS-----IGTVFRLGMDWHNTPVTVQNTASLSETS 440
475 YNVGVNVSLSGSDNRDEYVNTYVLEMTLADSTSTNATV---HLDG 532
441 THK 443
533 THF 535

RESULT 6
US-10-092-0506-98
Sequence 98, Application FC/TGS0405068
GENERAL INFORMATION:
TITLE OF INVENTION: Enzymes Having Alpha Amylase Activity
TITLE OF INVENTOR: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 05010-00000
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/270, 495
PRIOR APPLICATION NUMBER: US 60/270, 496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291, 122
PRIOR APPLICATION NUMBER: US 60/055, 779
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FastSeq for Windows version 4.0
SEQUENCE:
LENGTH: 376
TYPE: PRT

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Db 623 BSSJGFLKDSNPNFN-----VLLMLLTD-----YLLITQNNAYLETKLYN 672
 QY 440 STRENGP 445
 Db 673 STRENGP 678

RESULT 8
 US-09-721-456-187
 SEQUENCE DESCRIPTION: SEQ ID NO: 187:
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Ligner, Joachim
 Chapman, Karen B.
 Morin, Gregg B.
 Andrews, William H.
 TITLE OF INVENTOR: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549
 FILING DATE: 01-OCT-1997
 FILING DATE: 01-OCT-1997
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US/08/846,017
 FILING DATE: 15-APR-1997
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/912,643
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: US/08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17865
 FILING DATE: 01-OCT-1997
 ATTORNEY/INVENTOR INFORMATION:
 NAME: Apple, Randolph; Ted
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION: (415) 576-0300
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1007 amino acids
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

Db 623 BSSJGFLKDSNPNFN-----VLLMLLTD-----YLLITQNNAYLETKLYN 672
 QY 440 STRENGP 445
 Db 673 STRENGP 678

RESULT 9
 US-09-721-456-110
 SEQUENCE 110, Application US/09721456
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Ligner, Joachim
 Chapman, Karen B.
 Morin, Gregg B.
 Andrews, William H.
 TITLE OF INVENTOR: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549
 FILING DATE: 01-OCT-1997
 FILING DATE: 01-OCT-1997
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US/08/846,017
 FILING DATE: 15-APR-1997
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/912,643
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: US/08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17865
 FILING DATE: 01-OCT-1997
 ATTORNEY/INVENTOR INFORMATION:
 NAME: Apple, Randolph; Ted
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION: (415) 576-0300
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1007 amino acids
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear


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US-10-092-411A-3159
/ SEQUENCE 3159, Application US/10092411A
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS
/ TITLE OF INVENTION: EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 032785-101 US/10/092-411A
/ CURRENT FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: US 09/134,001
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ NUMBER OF SEQ. IDS NOS: 5676
/ SEQ. ID NO 3159
/ TYPE: PR
/ ORGANISM: Staphylococcus epidermidis
/ QUERY MATCH 4.4%, Score 105; DA 6; Length 10182;
/ Best Local Similarity 21.2%; Pred. No. 71;
/ Matches 121; Conservative 71; Mismatches 202; Indels 176; Gaps 28;
/ 6 NIFSNTSLGDLINMEYFNINISKLSIQHKN-TLVDSOTMAEVSREDVQLAP- 62
/ 1313 NSGIVTVITKGLDKEFSSGSLANWYLAHNDIILISWKSILQNGYGLDHPD 1372
/ 63 ---IFFPKFGLSGSDGRVITVO---NEIIVYH---SWTEFSISPRIR--- 105
/ 1373 HSLVITLQATLQNGDNLVLLQATANSLSINSEKLAEGNSGYSKIFED 1432
/ 106 ---NMYVSMLPTSIDSVKANSMSGIIISNLFYFLKQNZSDSISFYDLSNNKP 162
/ 1433 DQKSTSLANSPIQDLVFNPIGDSQSHSVI---YKNSSTVWQVPAANGASA 1489
/ 163 YH--RWFYFVFN--WGS-----NKKITMKGLDITVY 193
/ 1490 FHDYRYKVAANNGIMVYKALYAPISPKVYIKELQGLSNTNIVYIVFVSRYK 1549
/ 194 KE-----LEGINKETFEENKIPFQGLSOSQSNKMTDORTFAKGLS 241
/ 1550 NPSIVTQNDHIVYGEFFETINVNDQTLNATVSDS--ATWNNEN---NBLG 1603
/ 242 KQNLINLSQGLTYWK--QWPKNDLYRNEYKTYWYDYLN--RYWAKNSQL-- 293
/ 1604 QAPVTV--NSIMIKYKATDKSNGESVS---PTNFKYKFKRTISSNOPYRIS 1659
/ 294 TERNNH---DFN-----BSVAILKRLGNVNTGVGGDILFDMILNNKATLPMK 343
/ 1606 IONKMSGSDIOWKWSLSMTLGLTNTYNSNNVHOSVYKNSGNNATVY--- 1716
/ 344 NMTADW-----NHSIEDTIA----- 359
/ 1717 -TTFSSGTHIVYVWVHLEVPVTVTFTVYVGGQFPFGKTSFSGVPLRFGVDAR 1775
/ 360 -ICGABGTQDNDN-----IIF-QIDPM-INPTTAS---QIFENNNEN 399
/ 1776 IWNQKQDQINSQJGSDLTHAKITFCQETTP-ROSTVYLSQGLPIQTLTNG-- 1833
/ 400 ISGCSIGTGYFELGSDGRNLYLVPTQY 429
/ 1834 -----RFSNGDAVFNQVQAVND 1852
/ RESULT 12
/ SEQUENCE 3154, Application US/10092411A
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ FILE REFERENCE: 032785-101
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 09/134,001
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ NUMBER OF SEQ. IDS NOS: 5676
/ SEQ. ID NO 3154
/ TYPE: PR
/ ORGANISM: Staphylococcus epidermidis
/ QUERY MATCH 4.4%, Score 104.5; DA 6; Length 497;
/ Best Local Similarity 21.3%; Pred. No. 1.7;
/ Matches 83; Conservative 51; Mismatches 153; Indels 103; Gaps 20;
/ 22 EFVFNDSKSLISQNGRNTLVDSOTMAEVSREDVQLAPFPFPLGSSGSEKAVI 81
/ 128 EBFNHLNDLQDLKH---DVSGYK-----FMLESIASIFSTSTGQKAPVQ 375
/ 83 VTQENYVNSYFSSISFPIRKINVSLSLPGVITLDSVYNSKNSI---GLISNLFV 138
/ 179 TNNKLASQKQSGLOFGE---QNTVWLSVPIH-----SCUSIVHARTVETFR 225
/ 138 TGL--ONESDSINFSISNNA--PKYKVFVYVNNMKNKIYNG---KLID 189
/ 225 LYKVFQDQNTWK-TTPTHNSLVPTLNMJLMDKGLTQPSLEVLXGLQGLMLPOLL 284
/ 190 ---TIKVELKIDGNSKIFTEFNKIP-----DGLTIGSDINNMWJDTFPAK-E 239
/ 385 QALTYVTVYNSQVETCSQFLTASQWKEKEDT--VQPSFVYKLNPNVANGCE 342
/ 239 LQGNQNLIFSLSATNVVQVNDQVNNYKNTVWIDVNTYNSVNSQIVNTFERN 398
/ 343 LLIGENVN-NQVLPKLAQTFQND-QTQDQGLAED----- 379
/ 390 NQFNDYVITIKLIGNNNTGVGGDILFDMITNNKALPMKMTWYVNNSTDIY 356
/ 380 ---DSQVYIVDR---SKDILSGENYI-----PVQI---ETIAQEGIEDAV 420
/ 359 ATGLRQ-----HLSNINIQP 376
/ 421 CVGISDQSGVPIVYVTVNDQINQTELIE 450
/ RESULT 13
/ SEQUENCE 3154, Application US/10092411A
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ FILE REFERENCE: 032785-101
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 09/134,001
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ NUMBER OF SEQ. IDS NOS: 5676
/ SEQ. ID NO 434
/ TYPE: PR
/ ORGANISM: Staphylococcus epidermidis
/ US-10-092-411A-3141

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Db 384 LNDLYEKEKESVDIEQNKETIDETPTPEEDALVYSKLR----- 430
Oy 327 LYFDMTHNNANLW-----KNETMAUNSTEDTALGRLQTDIMONI 373
Db 431 VVULSLEK--ELQCCGAGIPOINWKTIVYR--WNGSTIDGISTQVEEDYF 485
Oy 374 IFQOPNNRYTVAQIFKSNFNEAI-----SGICSIGT 408
Db 486 LAHLKNNVSVAVNGL--TUPFSINIHOINQLRGDVSQT 527

Search completed: November 7, 2002, 14:53:14
Job time: 20 secs

GenCore version 5.1.13
Copyright (c) 1993 - 2002 CompuGen Ltd.

CM protein - nucleic search, using frame_plus_22n model

Run on: November 7, 2002, 16:32:06 : Search time 2721 Seconds
(Without alignments)
4813.033 Million cell updates/sec

Title: US-09-910-186A-10
Sequence: 1 MYTFPNTSTNMSLADLI.....NVAELSTSTHNPVYVSE 450

Scoring table: BLOSUM62
Gapop 10.0, Xgapop 0.5
Fgapop 6.0, Ygapop 7.0
Delop 6.0, Delxet 7.0

Searched: 205640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109380

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-b=GENEID -f=FASTA -s=FASTA -t=FASTA -u=FASTA -v=FASTA -w=FASTA
-x=FASTA -y=FASTA -z=FASTA -aa=FASTA -ab=FASTA -ac=FASTA -ad=FASTA
-ae=FASTA -af=FASTA -ag=FASTA -ah=FASTA -ai=FASTA -aj=FASTA -ak=FASTA
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-zy=FASTA -zz=FASTA

Database :

GenBank:
2: gb|acc.*
3: gb|acc.*
4: gb|acc.*
5: gb|acc.*
6: gb|acc.*
7: gb|acc.*
8: gb|acc.*
9: gb|acc.*
10: gb|acc.*
11: gb|acc.*
12: gb|acc.*
13: gb|acc.*
14: gb|acc.*
15: gb|acc.*
16: gb|acc.*
17: gb|acc.*
18: gb|acc.*
19: gb|acc.*
20: gb|acc.*
21: gb|acc.*
22: gb|acc.*
23: gb|acc.*
24: gb|acc.*
25: gb|acc.*
26: gb|acc.*
27: gb|acc.*
28: gb|acc.*

Prod. NC. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2886	99.8	4779	CSPHCL1	X53751 Clostridium
2	2886	99.8	4779	CSPHCL1	X53751 Clostridium
3	2886	99.8	4779	CSPHCL1	X53751 Clostridium
4	2886	99.8	4779	CSPHCL1	X53751 Clostridium
5	2886	99.8	4779	CSPHCL1	X53751 Clostridium
6	2886	99.8	4779	CSPHCL1	X53751 Clostridium
7	2886	99.8	4779	CSPHCL1	X53751 Clostridium
8	2886	99.8	4779	CSPHCL1	X53751 Clostridium
9	2886	99.8	4779	CSPHCL1	X53751 Clostridium
10	882.5	36.9	4043	CLOE8	D49440 Clostridium
11	882.5	36.9	4043	CLOE8	D49440 Clostridium
12	882.5	36.9	4043	CLOE8	D49440 Clostridium
13	882.5	36.9	4043	CLOE8	D49440 Clostridium
14	882.5	36.9	4043	CLOE8	D49440 Clostridium
15	882.5	36.9	4043	CLOE8	D49440 Clostridium
16	882.5	36.9	4043	CLOE8	D49440 Clostridium
17	604.5	25.3	3937	CHEONG1	X74162 Clostridium
18	604.5	25.3	3937	CHEONG1	X74162 Clostridium
19	604.5	25.3	3937	CHEONG1	X74162 Clostridium
20	604.5	25.3	3937	CHEONG1	X74162 Clostridium
21	602.5	25.2	3876	AF29526	AF29526 Clostridium
22	554.5	24.9	4759	AF29526	AF29526 Clostridium
23	554.5	24.9	4759	AF29526	AF29526 Clostridium
24	554.5	24.9	4759	AF29526	AF29526 Clostridium
25	554.5	24.9	4759	AF29526	AF29526 Clostridium
26	554.5	24.9	4759	AF29526	AF29526 Clostridium
27	554.5	24.9	4759	AF29526	AF29526 Clostridium
28	554.5	24.9	4759	AF29526	AF29526 Clostridium
29	554.5	24.9	4759	AF29526	AF29526 Clostridium
30	554.5	24.9	4759	AF29526	AF29526 Clostridium
31	554.5	24.9	4759	AF29526	AF29526 Clostridium
32	554.5	24.9	4759	AF29526	AF29526 Clostridium
33	554.5	24.9	4759	AF29526	AF29526 Clostridium
34	554.5	24.9	4759	AF29526	AF29526 Clostridium
35	554.5	24.9	4759	AF29526	AF29526 Clostridium
36	554.5	24.9	4759	AF29526	AF29526 Clostridium
37	554.5	24.9	4759	AF29526	AF29526 Clostridium
38	554.5	24.9	4759	AF29526	AF29526 Clostridium
39	554.5	24.9	4759	AF29526	AF29526 Clostridium
40	554.5	24.9	4759	AF29526	AF29526 Clostridium
41	554.5	24.9	4759	AF29526	AF29526 Clostridium
42	554.5	24.9	4759	AF29526	AF29526 Clostridium
43	554.5	24.9	4759	AF29526	AF29526 Clostridium
44	554.5	24.9	4759	AF29526	AF29526 Clostridium
45	554.5	24.9	4759	AF29526	AF29526 Clostridium

ALIGNMENTS

RESULT 1

[illegible]

[illegible]

175 MchMcGlyAsnMetAspTyrThrIleSerGlyAsnIleAspThrIleGlyValLys 124
 3031 ---TCGATACCACTTAATAATTAATTAATGTAAGTACGATCAATCAATAGATAGATAGA 3087
 195 GluLeuThrGlyIleLeuPheSerIleThrIlePheGluIleAsnGlyIleProAsp 214
 3088 GATATAGAGAGATTAATGCTAATGATGAATATATATTAAATTAGAT----- 3135
 215 ThrGlyLeuIleThrSerAspSerAspIleAsn-----MetTyrIleAsp 230
 3136 -----GSTATATAGATAGACACACACATTCATTCTGGATGAA 3171
 231 AspPheTyrIlePheAlaLysGluLeuAspGlyLysAspIleAsnIleLeuPheAsnSer 250
 3172 TATTTCGATATTTTAAATACGAAATTAAGTCATCATCATATGACGAAATATTAAT 3231
 251 LeuGlnTyrThrAsnValIleAspTyrTrpGlyAsnAspLeuAspTyrAsnGlyGlu 270
 3232 CAATCAATACGCAATATTAAAGATTTTGGGAAATCTTAAATGTAAGAGAGAA 3291
 271 TyrTyrMetValanIleAspTyrIleAsnAspTyrMetTyr-----AlaAsn 286
 3292 TATTATGCTATTATGCGGAAATAAATCTATATTAACTTAAGTAAGATGATCTCT 3351
 287 SerATGCTIleValPheAsnThrArgATArgAsnAsn----- 299
 3352 GTAGCTGAATTTTACACGTAGCAATAATATCAATCAATTCGATATATAATATAGA 3411
 300 AspPheAsnGluGlyTyrGlyIleIleValIleAspArgLeuGlyAsnThr----- 316
 3412 GATTATATATCGGAAAAATTTATTATAGAAGAA--AAGTCAATTCCTCAATCTATA 3468
 317 AsnAspThrAsnValLysGlyLysAspGlyLeuTyrPheAsnMetThrIleAsnAspLys 336
 3469 ATGATGATATAGTATAGAAAGAGAGATATATATATCATGATTTTTTAAATTAAATCAA 3528
 337 AlaTyrAsnLeuPheMetLysAsnGluThrMetTyrAlaAsnHisSerThrGluAsp 356
 3529 GAGTGGAGATATATATG----- 3546
 359 TleTyrAlaIleLysLeuArgGluGlnThrLys-----AspIleAsnAspAsn 372
 3547 ---TATTAATATTTTACAGAGAGAGAGAAATATGTTTATGCTCTATATAGTATCT 3603
 373 IleIlePhe-----GlnIleGlyProMetAsnAsnThrTyrTyrTyrAlaSer 388
 3604 GATGACTTTACATATCTACAAATTAAGAGATATGTCACACCAACATATGTTGT 3663
 389 Gln---IlePheLysSerAsnPheAsnGlyLeuAnIleSerGlyIleCysIleGly 407
 3664 CAGTGGCTTTTTTAAAAA-----GATCGAGATATCTCATGAGAGATAGGATATATG 3717
 408 ThrTyrAspPheAsnGlyGly----- 415
 3718 ATTCAGTCTTTGACATCTGGATATGCTATTTAAGATATAAAGATATATTTTGATATA 3777
 416 ---AspTyrTyrArgIleAsnTyrLeuValProThrValLysGluIleAsnTyrAlaSer 434
 3778 AGTAATAGTATAC-----TAAAGAGATTAAGAGAAACCAATATATCA 3822
 435 LeuLeuGluIleThrSerThrIleTyrGlyPheValProValSerGlu 450
 3823 AAATATG-----GATGTAAATGCGCATTTATCTTAAGATGAA 3861

Search completed: November 7, 2002, 18:38:07
 Job time : 2772 secs

This is the DNA sequence of the Clostridium botulinum serotype C1 (Stockholm strain) neurotoxin fragment C gene contained in plasmid His-tagged N-terminal extension. The vector was used to express native (i.e., non-fusion) soluble C fragment in Escherichia coli host strains. The recombinant toxin was purified by ion exchange chromatography. C-botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Cell-referenced cells and yeast cells. The recombinant toxins are used as immunogens for the production of vaccines and antitoxins that are effective against humans and animals at risk of botulism. Intoxication with clostridial toxin.

Sequence 1502 BP: 600 A; 135 C; 249 G; 496 T; 0 other:
Alignment Scores:
Pred. No.: 4,676-139 Length: 1502
Identical Similarity: 98.66% Conservative: 339
Percent Similarity: 98.66% Conservative: 339
Best Local Similarity: 97.99% Mismatches: 5
Entropy Match: 36.99% Gaps: 0

DNA:

US-910-186A (1-430) x AVX305B (2-1502)

OY 4 ProPhenAlaLePheSerTy-ThrAsnSerSerLeuLeuValAspIleAsnGluTy 23
OY 135 CUNATACAGCGTCGTATCATGCCTACATGGCCTTATTAAAGAAATATATAGATGA 211
OY 23 PHeAsnAlaLeuAspSerTyIleSerLeuLeuLeuAsnGlyAsnThrIleVa 43
OY 213 TTATTTATATATATGTCCTTAAATTAATTTAGCTTAAAGCAAAAAGCTTAGT 271
OY 43 IAspThrSerGlyTrpAsnAlaValSerLeuGluGlyAspValcIleAsnProI 63
OY 277 GATATCANGATATATAGAGAGAGATGATGAGAGCGATGTCTAGCTTATCCAT 331
OY 63 ePhoProbaAspHisLeuValSerLeuGluGlyAsnGlyValcIleAsnThr 381
OY 332 ATTCTCATTTACTTAAATTAGCTAGCTAGCGAGAGAGAGATAGTATAGTAAAC 391
OY 83 rGlabaLeuAsnTrileValTythrAsnSerTytyrGluSerPheSerIleSePepI 103
OY 394 CGAGAAGAAATATATATATATCTATATATTAAGGTTTTTGACATAGTTTGGAT 451
OY 103 eArgIleAlanuTytyrPalSerAnuLeuProGlyTytyrIleIlempSerValyaa 123
OY 452 TAGATAATATATATAGTATAGTTTACCCTGGATATATCTATATATAGTATAAA 511
OY 123 ManSerTytyrPserIleGlyIleIleSerAsnPhelValPheThrLeuLyasna 143
OY 512 ThCTCCTAGCTAGCTAGCTAGCTATATATATATATATATATATATATATATAT 571
OY 143 nGluAspSerGluGlnSerIleAsnPheSerTytyrIleAsnAlaAlaProGlyTy 203
OY 572 TGAGAT 631
OY 163 AsnLysTyPhePheValThValThrAsnAsnMetGlyAsnMetTyIlePyrI 183
OY 632 CAAT 691

PI XE XX
XX 3275 AAAGATG 3337
OY 265 GIVASASPGLAKTYTVASNYGLGVYTVetValAsnHlAsnPytLeuAsnAg 281
DX 338 GGAAATGATTTAGAAATATATATATATATATATATATATATATATATATAG 3397
PT 288 TyrMeTVaTVASNAsArGdLIILeVAlPheAsnTrAAsArAsnAsnAspPhe 301
OY 398 TYNIHTITGCGMCTCACARCAATGTTTTTATACAGCTAGAAATATATAGCTC 3457
DX 320 ASDGLQGYTYRYSLEILETLEYASGLTEARGVAsnThrAsnAspPhuArVal 321
OY 345 ATATAGAGAT 3517
DX 322 ARdGIgAPfIleLeuTyPheAsmThrIleAsnAnilyAlaTyAsnLeuPhe 341
OY 3516 CAGAGAGAT 3577
DX 341 MetTyPheGluGlnMetTytyrAspAsnMetIleSerMetLeuAspPytyrAlilegly 361
OY 3578 ATGAGAGAGAAAT 3637
DX 367 LeuArGluGlnTrpAspIleAsnAspHlIlePheGluGlnProMetAsn 381
OY 3638 TTAGAGACACAAGAGATATATATATATATATATATATATATATATATATAT 3697
DX 381 ASnThyTyTVtVALSerGlnIlePheLysSerAmPheAcylGluAsnIleSer 401
OY 3698 ATACTAT 3757
DX 402 GlyIleGlySerIleGlyTytyrAspPheALeuglyGlyAspTytyrAsnAla 421
OY 3758 CGATPAGAT 3817
DX 422 TyrLeuValProThValValGlyAsnTytyrAlaSerIleGluSerThr 441
OY 3818 TTATGAG 3877
DX 442 HisTrpIClPheValProValSerdlu 450
OY 3878 CATGGGATTTTGGATAGTAA 3904
OY 4 AVX305B
OY 4 AVX305B standard; DNA; 1502 BP.
AVX305B8;
AVX305B8;
07-DEC-1998 (first entry)
Clostridium botulinum type C1 toxin C fragment gene in pETHisb.
Antitoxin; vaccine; neurotoxin; toxin C; intoxication; immunogen;
Soluble; PCR; ds.
Synthetic.
Clostridium botulinum serotype C1 Stockholm strain.
Location/Qualifiers
KEY 108_1463
CD 108_1463
FN /clp-a
OS W09808540-A1.
PN 05-MAR-1998.
PX 28-AUG-1997; 97NC-U951594.
XX 28-AUG-1996; 96GS-0704159.
XX (CPRI)- OPHIDIAN PHARM INC.

[illegible][illegible][illegible]

Copied from 10910136 on 05-05-2004

GenCode version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

ON protein - nucleic search, using frame_plus_22n model

Run on: November 7, 2002, 17:45:26 Search time 54 seconds
File: us-09-910-186a-10
Perfect score: 2391
Sequence: 1 MTFPMFTSTNLSKLDI.....NTASLLRSTHRGVPVWSE 450
255:640 Million cell updates/sec

Scoring table: BLOSUM62

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APPLICATION NUMBER: US 08/139,154
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/161,907
 PUBLICATION NUMBER: US 6,193,593
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/985,321
 PUBLICATION NUMBER: US 6,486,992
 PUBLICATION DATE: 04-DEC-1992
 APPLICATION NUMBER: US 07/439,751
 PUBLICATION DATE: 31-OCT-1989
 INVENTOR:
 NAME: ANGLIA, DIANE E.
 TELEPHONE: (415) 705-8410
 TELECOMMUNICATIONS INFORMATION:
 TELEPHONE: (415) 705-8410
 REGISTRATION NUMBER: 40,027
 INVENTOR'S ADDRESS:
 TELEPHONE: (415) 397-8338
 TELEFAX: (415) 397-8338
 INVENTOR'S ADDRESS:
 LENGTH: 3891 base pairs
 STRAND: sense
 STRAND: antisense
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 NAME/KEY: CDS
 LOCATION: 1..3888
 ORF: 480-604:27
 Weight Scores:
 Id. No.: 3891
 Length: 3891
 Cons: 82
 Conservative: 82
 Similarity: 46.94%
 Local Similarity: 31.57%
 Indels: 186
 Mismatches: 95
 Gaps: 11

3 1leprpPhaSerLlePheSerThrAndSerLeuLysAspLleAsnGlu 23
 25 ATCTTCCTTCCTCCAAATAGAGATATACAGATATATATACATCTACTGAA 2604
 23 ThrPheAsnThrLleAsnSerLysLleSerLeuLleAsnAspLysAsnThrGlu 42
 24 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 2605
 2605 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 2664
 43 ValAspThrSerGlyThrAsnAlaGluValSerGluGluValGluLleAsnPro 62
 2655 AATGACTTACAGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2724
 63 1leprpThrPheSerPheSerPheSerPheSerPheSerPheSerPheSerPheSer 79
 2725 ATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2769
 80 ValLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 99
 2770 ATGAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2829
 100 SerPheThrLleLleLleLleLleLleLleLleLleLleLleLleLleLleLle 116
 2830 AGCTTTGGTATGAGTATCTCTGATTTTAACTGATTTTAACTGATTTTAACTGAT 2869
 117 1leprpSerValLleAsnAspSerGlyThrSerLleGlyLleLleSerAspPheLle 136
 2890 ATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2949
 137 ValPheThrLleGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 156
 2950 ATCTGGCTTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3009
 157 SerAsnAspLysProGlyThr---AnnLysThrPhePheValThrValThrAsnMet 175

3010 ATGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3069
 176 MetGluAsnMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 185
 3070 TTTAATGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3129
 177 ValPheThrLleLleLleLleLleLleLleLleLleLleLleLleLleLleLle 215
 3130 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3189
 216 GlyLysLleThrSerAspSerAspAsnLleAsnMetThrLleAspPheThr 235
 3190 ---CATGATATATTTGGATTAATAATATTTAACTTTTAACTTTTAACTTTT 3225
 236 AlaLysGluLysAspGlyLysAspLleSerLleLleLleLleLleLleLleLle 255
 3226 GATAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3285
 256 ValMetGluAspGlyThrGlyValAspLysLysLysLysLysLysLysLys 275
 3286 ATTTAAAGAGCTTTGGGGTGATTTATCATATATATATATATATATATATAT 3345
 276 1leAspThrLleAsnA-GlyMetThrLysLysLysLysLysLysLysLysLys 287
 3346 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3405
 288 ---ArgLleValPheAspThrArg---ArgAsnAsnAspPheAsn 302
 3406 CTTAAAGGGCTAGAGTAGGATGATGATGATGATGATGATGATGATGATGATG 3465
 323 GlyLysLleLleLleLleLleLleLleLleLleLleLleLleLleLleLle 342
 3426 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3529
 343 LysAsnGluThrMetThrLysLysLysLysLysLysLysLysLysLysLysLys 362
 3580 ---GCTACTATGCTACAGGACAGGCTGAGAAAAATATCTAGT 3621
 363 ArgGluGluThrLysAspLleLleAspAsnLleLlePheGluLleLleLleLle 382
 3622 GCATTAATATACCTGATAGGAATCTAGTCACTGATGATGATGATGATGATG 3681
 383 ThrGlyThrValSerGluLlePheSerMetAspGluGluLysLleSerGly 402
 3682 GCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
 403 1leCysSerLleGlyThrThrArgPheAspLysGlyLysLysLysLysLys 422
 3739 ATGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3771
 423 LeuValProThrValLysGluGlyValLysThrValSerLleLysLysLys 440
 3772 ATGCTTAACTAGTACAGATGATGATGATGATGATGATGATGATGATGATGAT 3831
 441 ---ThrHisThrPheValProValSerGlu 450
 3832 TTGGGTTCCTGCGAATATTTCTCTGTATGATGAT 3867

RESUB 2
 ; 09-456A-27
 ; Sequence 27, Application US/08405496A
 ; Patent No. 5918665
 ; GENE: CLOSTRIDIUM BOTULINUM
 ; APPLICANT: WILLIAMS, JAMES A.
 ; TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
 ; TITLE OF INVENTION: NEUROTOXIN
 ; CORRESPONDENCE ADDRESS:

Dy 3772 ATACCAATACAGCAAGTATGATATGATATGACAAATAGAGAGCTAGAGGACT 3891

Dy 441 -----ThrsitrgpVheIpaPwalserglu 450
Dy 3832 TGGCGTCTCATGGGAATTTATCTGTATGAT 867

RESULT 3

US-08-915-136-27

; Sequence 27, Application US/08915136

; Patent No. 6290961CEN

; APPLICANT: KIM, JOHN A.

; APPLICANT: THALLEY, BRUCE S.

; APPLICANT: KIM, JOSEPH R.

; APPLICANT: EYRA, JOSEPH R.

; APPLICANT: STAFFORD, DOUGLAS C.

TITLE OF INVENTION: VACCINE AND ANTIOXIN FOR TREATMENT AND

PREVENTION OF ACUTE AND CHRONIC C. DIFFICILE DISEASE

NUMBER OF SEQUENCES: 31

INVENTOR: JOHN A. KIM, JOHN A. KIM, JOSEPH R. EYRA, DOUGLAS C. STAFFORD

CORRESPONDENCE ADDRESS: 1400 CALABASOIL, 14P

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC-compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC-compatible

CURRENT APPLICATION ID: Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/915,136

FILING DATE: 08/09/1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/460,504

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/405,496

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/329,154

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/161,907

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/985,321

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/439,791

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/189,000

ATTORNEY/AGENT INFORMATION:

NAME: INCOLA, DIANE E.

REFERENCE/DOCKET NUMBER: OPND-01763

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 397-8110

TELEFAX: (415) 397-8138

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

STANDARD: double

STANDARD: double

STANDARD: double

STANDARD: double

STANDARD: double

STANDARD: double

STANDARD: double

STANDARD: double

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STANDARD: double

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STANDARD: double

Prod. No.: 3,46e-53 Length: 3891
Score: 586.50 Matches: 249
Percent Similarity: 31.54% Complement: 346
Query Match: 24.53% Mismatches: 55
Dy: 4 Gaps: 11

US-09-910-186a-10 (1-450) x US-08-915-136-27 (1-3891)

Oy 3 lleoPhenleheSeThraenSerleuLeuysAspIleleandgu 22

Dy 2545 ATACTTTCAGCTTCCCAATAGTACTAGTAAATATTCATCAATCTACTGAA 2604

Oy 23 ThPheAsnleleleSeSerlyleleuSerleuLeuAsnGlyAspThrleu 42

Dy 2605 TTTATGAAATATATATCTCTATGATTAATGATATGAATGATATCAATTA 2664

Oy 43 ValAspThrSerGlyIleValAsnGluValSerGluGluAspValGluLeuAsnPro 62

Dy 2665 ATGACTCTGATGATCATCAATAAATAAATATGTTAGTAAGTAATTTGATCCA 2724

Oy 63 lleoPhetOphap-----PheylSeuSerGlyLysAspGlyLys 79

Dy 2725 ATGATAAATCAATCAATATATTTATTTAGAGTGT-----NAK 2769

Oy 80 ValIleValThrGlnAsnGluAsnIleValIleAsnSerMetTyCLeuSerPheSerIle 95

Dy 2770 ATTCGGGTATTTTAAATAATCTTATGATATATATGATATGATATGATATGAT 2829

Oy 100 SerPheThrIleAsnGlyIleAsnGlyIleValSerAsnLeuPro-----GlyTThr 116

Dy 2830 AGCTTGGATATATATCTCTAGTATTTTACATATGATGCTATTAATGATATCA 2889

Oy 117 lleleGepSerValIysAsnAsnSerGlyIleSerIleIleSerAspPheleu 136

Dy 2890 ATATAATGATGGAATATATCAGAGGAAGTACTTAATATGTTGAAATA 2949

Oy 137 ValPheThrIleGlyGlnAsnGluAspSerGluGlnSerIleAspPheSerTyAspIle 156

Dy 2950 ATCTGGCTTTACAGGATCTACAGAAATAAACAAGAGTAGTTTAAATACAGTCA 3009

Oy 157 SerAsnAsnAlaProGlyIleTy-----AsnGlyIlePheValIleValThrAsnAspMet 175

Dy 3010 ATGATATCTACAGATATATTAACAGATGGTATTTTGTATCTACTCATATATGA 3069

Oy 176 MetGlyAsnMetIleIleTyIleAsnGlyIleValAsnIleAspThrIleValGlyIle 195

Dy 3070 TTAATATCTTAAATTTATTAATATGAGATATCAATCAAAACATCAATCAAT 3129

Oy 195 LeuThrGlyLeuAsnPheSerIleThrPheIleGluLeuAsnLysIleProAspPhe 215

Dy 3130 TTAGTATATCTCACTGCTATGATATATATATATATATATATATATATATAT 3189

Oy 216 GlyLeuIleThrSerAspSerAspAsnIleAsnMetIleAsnGlyIlePheIle 235

Dy 3190 -----CATGATATATTTGGATATATATTTAACTTTT 3225

Oy 236 AlaIysGluLeuAspIlyIleAspIleMetIleAsnIlePheAsnSerLeuIleTyThrAsn 255

Dy 3226 GATAGGAATATATTAAGAAGATCAAGATATATGATATCAATCAATCAATCACT 3285

Oy 286 ValIleValAspTyIlePdyIleAsnAspLeuAsnGlyIleTyIleTyIleAsnValSer 275

Dy 3286 ATTTTAAAGATTTTGGGTGATATTTACATATATTAATCAATCAATCAATCAAT 3345

Oy 276 lleoGlyTyLeuAsnAspPhePheTyIleAsnIleAsnSer----- 287

Dy 3346 TTTATGATCACTAAATATATGCTATGATTAATATATGATATGATATGATAT 3405

Oy 288 -----AspGluIleAsnIlePheAsnGlyIleAsn 302

Dy 3405 CTTAAAGGGCTAGAGGTAGCTGTATGATCAATCAATCAATCAATCAATTTGAT 3465

[illegible][illegible]

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570 GATATCTCCAAATCTACATCAACGGCTGTGTCACGACGAGAACGATCTCATCT 629
136 GTTTCGTTTAAATPheSerLysThrIleThiPheSerLysIlePheSerThrIle 219
610 GGTACATCAACGCTGTCTTCAATCATCTTCAACGACAGCTGTGGAGACT 687
216 YGAILethSerAspSerAspSerLysSerLysIlePheSerThrIlePheSer 236
668 -----CACCGTACACTGGATCAACATCTCATCTGTGTGCA 725
216 ALYGLuLeuAlaGlyLysAspIleSerLysLeuPheSerLysIleThrIleAsn 756
726 CAAGATCTCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 795
216 IVALYAspTyrTTPGIAsnAspLeuTyrTAsnLysGlyTyrTAsnValAsnIle 276
786 CCGAGAAATTCCTGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
216 AspTyrLeuAsnArgTyrMetTyrAlaAsnSer ----- 287
846 GTATACCCGAAATATATATATATATATATATATATATATATATATATATAT 905
288 -----ArgIleIleValPheSerThrArg---ArgAsnAsnAsnAsnPheSer 1303
906 GAAGCTCCGGCTGGCTGTCTGTGTAGATACCAACGATCTGCTGCTGCTGCTG 965
303 GGTyrTyrTyrIleIleLysArgIleArgIleArgIleAsnThrAspThrArgIle 123
966 TGATCAAAATCATCATCAAGAAATACGCTGTGTACAAAGAGCAATATGTTGSCAA 1025
323 GYGLYAspIleLysTyrPheSerPheThrIleAsnAsnLysAlaTyrAsnLeuPhe 123
1026 CATATGCTGTATACATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
343 SASGILuThiMetTyrAlaAsnAsnIleSerThrGluAspIleTyrAlaIleGlyLeu 363
1078 -----GCTCAATGCTCTCGAGCTGTGTGAGAAAGATCTGTCTCT 1121
363 GGLuIleThiLysAspIleAsnAsnIlePheIleIleGlnPheGlnPheAsnThr 383
1122 TCTGAATATCCGAGCTGTGTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
383 GTTyrTyrTyrAlaSerGlnIlePheLysSerAsnPheAsnGlyLysAsnIleSerGly 403
1192 CAGGGTATCATCAACATCC-----AAATATCTCTGACAGAACATGATCAATAT 1238
403 GYSerIleGlyTyrTyrAspPheArgPheAsnGlyLysGlyAspTyrTyrGlnIle 423
1239 GGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1271
433 VALProThrValLysGlyIleGlyAsnTyrAlaSerLeuLeuIleSerThrSer----- 440
1272 GCTAAATGCTGTCTCAACTGCTGATCATCTGATCATCTGATCATCTGCTCTCT 1331
441 -----ThiIleTyrPheValProValSerGlu 450
1332 GGGTCTCTCTGAGATTCATCCCGTTTATGAC 1365

```

RESULT 5

US-09-405-496A-25

Sequence 25, Application US/08405496A

GENERAL INFORMATION:

APPLICANT: WILLIAMS, JAMES A.

TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

INVENTOR: WILLIAMS, JAMES A.

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

```

ZFP: 94104
COMPUTER READABLE FORM:
MEDIAN TYPE: Flippy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/405-496A
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
PRIMER APPLICATION NUMBER: US 08/329,154
PRIMER APPLICATION DATE: 25-OCT-1994
PRIMER APPLICATION NUMBER: US 08/161,907
PRIMER APPLICATION DATE: 02-DEC-1993
PRIMER APPLICATION NUMBER: US 07/985,321
PRIMER APPLICATION DATE: 04-DEC-1992
PRIMER APPLICATION NUMBER: US 07/429,791
PRIMER APPLICATION DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
FAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 base pairs
TYPE: nucleic acid
STRANDNESS: double
MOLECULE TYPE: DNA (genomic)
FEATURE:
LOCATION: CDS
LOCATION: 1..1386
US-08-405-496A-25
Alignment Scores:
Pred. No.: 8,448-51
Score: 559.50
Matches: 147
Mismatch: 14
Indels: 56
Query Match: 23.14%
DB: 2
US-09-910-186A-10 (1-450) x US-08-405-496A-25 (1-1402)
4 PhePheSerIlePhePheTyrThrAsnSerLeuLysAspIleLeuGlyTyr 23
136 GTTTCGTTTAAATPheSerLysThrIleThiPheSerLysIlePheSerThrIle 219
610 GGTACATCAACGCTGTCTTCAATCATCTTCAACGACAGCTGTGGAGACT 687
216 YGAILethSerAspSerAspSerLysSerLysIlePheSerThrIlePheSer 236
668 -----CACCGTACACTGGATCAACATCTCATCTGTGTGCA 725
216 ALYGLuLeuAlaGlyLysAspIleSerLysLeuPheSerLysIleThrIleAsn 756
726 CAAGATCTCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 795
216 IVALYAspTyrTTPGIAsnAspLeuTyrTAsnLysGlyTyrTAsnValAsnIle 276
786 CCGAGAAATTCCTGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
216 AspTyrLeuAsnArgTyrMetTyrAlaAsnSer ----- 287
846 GTATACCCGAAATATATATATATATATATATATATATATATATATATATAT 905
288 -----ArgIleIleValPheSerThrArg---ArgAsnAsnAsnAsnPheSer 1303
906 GAAGCTCCGGCTGGCTGTCTGTGTAGATACCAACGATCTGCTGCTGCTGCTG 965
303 GGTyrTyrTyrIleIleLysArgIleArgIleArgIleAsnThrAspThrArgIle 123
966 TGATCAAAATCATCATCAAGAAATACGCTGTGTACAAAGAGCAATATGTTGSCAA 1025
323 GYGLYAspIleLysTyrPheSerPheThrIleAsnAsnLysAlaTyrAsnLeuPhe 123
1026 CATATGCTGTATACATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
343 SASGILuThiMetTyrAlaAsnAsnIleSerThrGluAspIleTyrAlaIleGlyLeu 363
1078 -----GCTCAATGCTCTCGAGCTGTGTGAGAAAGATCTGTCTCT 1121
363 GGLuIleThiLysAspIleAsnAsnIlePheIleIleGlnPheGlnPheAsnThr 383
1122 TCTGAATATCCGAGCTGTGTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
383 GTTyrTyrTyrAlaSerGlnIlePheLysSerAsnPheAsnGlyLysAsnIleSerGly 403
1192 CAGGGTATCATCAACATCC-----AAATATCTCTGACAGAACATGATCAATAT 1238
403 GYSerIleGlyTyrTyrAspPheArgPheAsnGlyLysGlyAspTyrTyrGlnIle 423
1239 GGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1271
433 VALProThrValLysGlyIleGlyAsnTyrAlaSerLeuLeuIleSerThrSer----- 440
1272 GCTAAATGCTGTCTCAACTGCTGATCATCTGATCATCTGATCATCTGCTCTCT 1331
441 -----ThiIleTyrPheValProValSerGlu 450
1332 GGGTCTCTCTGAGATTCATCCCGTTTATGAC 1365

```

RESULT 5

US-09-405-496A-25

Sequence 25, Application US/08405496A

GENERAL INFORMATION:

APPLICANT: WILLIAMS, JAMES A.

TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

INVENTOR: WILLIAMS, JAMES A.

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

CLASSIFICATION: 424
 PRIOR APPLICATION DATA
 FILING DATE: 25-OCT-1994
 PRIOR APPLICATION DATA:
 FILING DATE: 08-DEC-1994
 PRIOR APPLICATION DATA:
 FILING DATE: 08-DEC-1994
 APPLICATION NUMBER: US 07/985,321
 APPLICATION NUMBER: 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/429,791
 APPLICATION NUMBER: 1999
 ATTORNEY/AGENT INFORMATION:
 NAME: INGOLLA, DIANE E.
 REGISTRATION NUMBER: 40-027
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-3410
 INFORMATION FOR SEQ NO. 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1330 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 NAME/KEY: CUS
 MAPING TYPE: DNA (genomic)
 FEATURE:
 LOCATION: 22
 1..1314

Length: 1330
 Mismatches: 144
 Conservative: 144
 Percent Similarity: 48.80%
 Percent Local Similarity: 31.37%
 Mismatches: 180
 Conservative: 111
 Gaps: 2

us-09-910-186a-10 (1:450) * US-08-405-490a-22 (1:1330)

16 LeuValAspIleLeuAsnGluThrPheAsnIleAspSerValLeuSerLeu 35
 10 CUCUGCTACTCTACAGTACGATACAGACATCATCACTCCACCTGACCTG 69
 36 GLeuAsnGlyAsnThrLeuValAspThrSerGlyValAsnIleValSerGlu 55
 70 GCGTACAGATCCATCTACAGTACGATACAGACATCATCACTCCACCTGACCTG 129
 56 GlyAspValLeuAsnProIlePheProPheAsp-----PheValSerGlySer 72
 130 TCTCAAGATTAATCTGACGATACGATACAGACATCATCACTCCACCTGACCTG 189
 73 SerGlyLeuAsnGlyValLeuValThrGluAsnIleuAsnIleValSer 92
 190 TCC-----AAATCGAAGTATCTCGAAGATCTGATCGATCACTCT 234
 93 AsnThrGlySerPheSerLeuAspThrLeuValAsnIleValSerGlu 212
 235 AATGAGAAATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
 113 Pro-----GlyThrIleLeuAspValLeuAsnAsnSerGlyThrSer 329
 285 TCTCTGACATGATCAATCACTCACTCACTCACTCACTCACTCACTCACTCTCTCTCT 354
 130 GlyIleLeuAsnGluValPheThrIleuValAsnGluValSerGluSer 439
 355 TCTCTGACATGATCAATCACTCACTCACTCACTCACTCACTCACTCACTCTCTCTCT 414
 150 ILeuAsnPheSerValAspLeuAsnAsnAlaProIlyltyr---AsnIlysrPhePhe 468
 415 GTGTATCAATATCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCTCTCT 474

165 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 188
 175 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 208
 185 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 234
 195 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 258
 205 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 284
 215 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 308
 225 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 334
 235 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 358
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 265 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 434
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 305 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 534
 315 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 558
 325 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 584
 335 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 608
 345 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 634
 355 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 658
 365 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 684
 375 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 708
 385 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 734
 395 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 758
 405 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 784
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 425 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 834
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 445 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 884
 455 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 908
 465 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 934
 475 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 958
 485 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 984
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 535 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1108
 545 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1134
 555 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1158
 565 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1184
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 615 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1308
 625 ValIleValThrAsnAsnMetIlyAsnMetIlyAsnMetIlyLeuAsnIlyValLeu 1330


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OY 114 ---GlytyrThrIleLeuSerValAsnAsn---Serglytyr 127
DB 325 AARGNATGATCAAAATTAAGCTCTCAAGAAACAACTATCTCAACAGATCAAGCTGGTGG 384
OY 128 SerIleClyIleLeuSerAsnPhaValPheThrIleuysGluGlnGluSerGlu 147
DB 335 AGGTAATCAAAATTAAGCTCTCAAGAAACAACTATCTCAACAGATCAAGCTGGTGG 384
OY 148 GluSerIleAsnPhaSerValAspIleSerAsnAlaArgGlytyr---Asnlys 165
DB 445 AGCAATACATCTTAGG---GATTACTAGCAATTAATTAATTAATTAATTAATTAATTA 501
OY 166 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 561
DB 186 LysAlaGluAspThrIleuValLysLysGluThrGlyIleAsnPhaSerValPhe 205
OY 562 GCTACTTGGAGGAGCAAAATTAAGCTCTCAAGAAACAACTATCTCAACAGATCAAGCT 621
DB 206 ThrPheMetIleuAsnValIleProAspThrIleuIleThrSerAspSerAspIle 225
OY 622 AACTTAACATCAAGTAAAG---TGATTAATTAATTAATTAATTAATTAATTAATTAAT 657
DB 226 AsnMetThrPheAspPhePheIlePheAluLysGluLeuAspGlyLysPheIleAsn 245
OY 658 TACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 717
DB 246 LysIlePheAspSerIleuThrIleAsnValLysAspThrIleuLysAspLeu 265
OY 718 AANTTACACACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 777
DB 266 ArgTyrAsnValGlyTyrIleuValIleAsnIle---TGTATTAATTAATTAATTAAT 276
OY 778 CGATTAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 289
DB 277 ---AspTyrLeu---AsaArgTyrPheTyrAlaAsnArgGln 289
OY 838 AAATATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 897
DB 290 LLeuAlaPheAsnThrValGlyAsnAsnAsnAspPheAsnGluGlyIleIleIle 309
OY 898 AATATTAATTAAGAGGTATTAAT---GGATCAAAATTAATTAATTAATTAATTAAT 942
DB 310 LysArgIleGlyGlnIleAsn---AspPheAsnValGluGlyLysPheIleGlytyr 328
OY 944 AAATATTAACCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1002
DB 329 PheAspMetThrIleAsnAsnValAspThr---AsnLeuLeu---AsnLeuLeu 1040
OY 1003 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1062
DB 341 PheMetLysAsnGlnIleuThrIleuValAspAsnIleSerThrGluAspIleTyrAla 360
OY 1063 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1122
DB 361 GlyLeuArgGluGlnThrIleuAspIleAsnAspAsnIleIlePheGlnIleSerPhe 380
OY 1123 AAAAATTAAGCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1146
DB 381 AsnAsnThrTyrTyrTyrIleuSerGlnIlePheLysAsnAsnPheAsnGlyGluAsn 400
OY 1147 GGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1200
DB 401 SerGlyIleCysSerIleIleThrTyrArgPheArgGluGlyGly---Asn 416
OY 1201 TCT---TTAGACTAGTATGCTACCATGATTAATTAATTAATTAATTAATTAATTAAT 1257
DB 417 ---TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 1305
OY 1258 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1305

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OY 431 AnTyTAlaSerLeuGluGlyUserThrSerThrIleThrGlyPheValPheValSerGlu 450
DB 1306 ---TTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1341
RESULT 15
US-08-280-228-3
Sequence 3, Application US/0828028
GENERAL INFORMATION:
APPLICANT: Makoff Dr. Andrew J
INVENTOR: Makoff Dr. Andrew J
APPLICANT: Makoff Dr. Andrew J
APPLICANT: Fairweather Dr. Neil F
TITLE OF INVENTION: VACCINES
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & WANDERLY P.C.
CITY: 1100000, 3571694th Gible Road
STATE: Virginia
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, version #1.25
CURRENT APPLICATION DATA: 08/280.228
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PUBLICATION NUMBER: US 07/618,312
APPLICATION NUMBER: GB 8926832.0
FILING DATE: 27-NOV-1990
CLASSIFICATION: 435
PUBLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-163
TELEPHONE: 17011 816-4000
TELEFAX: (703) 816-4100
INVENTOR: 20099 NIXON DR
LENGTH: 1359 base pairs
SEQUENCE CHARACTERISTICS: 3
STANDARDNESS: double
TOPOLGOL: linear
MOLECULE TYPE: DNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1356
US-08-280-228-3
Alignment Scores:
Score: 6366-36
Matches: 420/60
Percent Similarity: 44.20%
Best Local Similarity: 25.20%
DB: 1.57%
Gaps: 1

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```

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;
; OTHER INFORMATION: primers used to introduce stu I and EcoR I
;
; OTHER INFORMATION: restriction sites into the 5' and 3' ends of the
;
; OTHER INFORMATION: BONT/A-L chain gene fragment

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Alignment Scores:			
Pred. No.:	7.6e-57	Length:	3894
Score:	588.50	Matches:	135
Percent Similarity:	49.3%	Conservative:	87
Best Local Similarity:	31.3%	Mismatches:	171
Query Match:	24.61%	Indels:	77
DB:	12	Gaps:	17

US-09-910-196A-10 (1-450) X US-10-051-952-9 (1-3894)

2	ThrltPheanllePheSerTyThrpaanserLeuLeuLysAspIleIleasn	21
2518	AGTATACCATTCATGCTCTTCTATATATACACGAGCACAAATTTTAAACAGGTTTAT	2577
21	GUTTyPheanllePheSerTyThrpaanserLeuLeuLysAspIleIleasn	21
2518	AGTATACCATTCATGCTCTTCTATATATACACGAGCACAAATTTTAAACAGGTTTAT	2577
2718	AATATATATATATATATAGTATGATATCTCTATTTATAGTTTAACTTATAGAGTGCGGCT	2637
42	LeuValaPheThrSerDysTyraaLaguLaaSerGluGluLysAspValGluIleuAsn	61
2618	TTATATATATCTTGGATATATGCTCAATGATATAGTGTGCGATGTATCTTTAT	2697
62	ProIlealPheThrPhePheLysSerSerSerSerSerSerSerSerSerSerSerSerSer	81
2618	TTATATATATCTTGGATATATGCTCAATGATATAGTGTGCGATGTATCTTTAT	2697
2698	GAATAGAGAAAGCTGCTATTTTATTTATTTATTTCT.....GAAATAGTAAATACG	2751
82	ValThrGluAsnGluIleValTyraSerSerSerSerSerSerSerSerSerSerSerSer	101
2752	GAACACAGAGAT	2811
102	TpplLeuAlaIleAsnTyItpValSerSer.....LeuProPheTy	115
2812	TGGGTAGGCTCTTAAT	2871
118	ThrIleGluAsnGluIleValTyraSerSerSerSerSerSerSerSerSerSerSerSer	135
2872	ACAT	2931
138	LeuValPheThrLeuLysIleAsnGluLysSerGluIleThrIlePheSerTyraaLagu	155
2932	ATATAGGATATATATAGTATCTTATCAATCAATCAATCAATTTTTCATATAGT	2991
158	IleSerAlaThrAlaProCysTy.....AsnGluLysPheValThrTyraaAsn	174
2992	ATAAGAAAT	3051
175	MetSerGluYaaMetLysTyItpValIleAsnGluLysLysIleAsnGluLysLysVal	194
3052	AGATATAGTACACCAAT	3111
195	GluLysIleThrLeuLysSerTyThrThrThrThrThrThrThrThrThrThrThrThr	214
3112	ACCTTATAGATATATATCTTAT	3171
215	ThrDysLeuIleThrSerAspAsnIleAsnMetTpIleAspPheTyIle	234
3172	ACTATCAATTT.....TTTGATATAGGATATATATAT	3207
235	PheAlaLysLeuLeuAspGluYaaAspIleAsnIlePheLeuLysIleLysProAsn	254
3208	TTTGATATAGGATATATATCTACAGATGCTCTCTATCTATATATATATATATATATAT	3267
255	MetValValYaaAspTyTpIleTyIleAsnAspLeuAspTyIleValTyIleMetVal	274
3268	AT	3327
275	MetIleAlaTyIleLeuAsnAlaTyMetTyIleValAsnSerArgIleValLeuAsnThr	294

[illegible]

005 10 Sequence 9, Application US/0051952-9
 1 Patent No. US5020261/1991A1
 2 Applicant: Wellcome, Patricia
 3 TITLE OF INVENTION: Methods of Administering
 4 FILE REFERENCE: 2933CIP
 5 CURRENT APPLICATION NUMBER: US/10/051,952
 6 PRIORITY APPLICATION NUMBER: 09/730,237
 7 PRIORITY APPLICATION NUMBER: 09/730,237
 8 PRIOR FILING DATE: 2000-12-05
 9 NUMBER OF SEQ ID NOS: 12
 10 SOFTWARE: Patentin Ver. 2.1
 11 SEQ ID NO 9: 8694
 12 TYPE: DNA
 13 ORGANISM: Artificial Sequence

Copied from 10910186 on 05-05-2004

Result No.	Score	Query Match	Length	DB	ID	Description
1	2391	100.0	1371	23	US-09-611-419K-9	Sequence 5
2	2391	100.0	1371	34	US-09-910-186A-9	Sequence 5
3	2386	99.8	3876	1	PC7-US87-1539A-59	Sequence 5
4	2386	99.8	3876	11	US-08-704-159-59	Sequence 5
5	2386	99.8	3876	42	US-10-203-315-5	Sequence 5
6	2386	99.8	3876	42	US-10-203-315-5	Sequence 5


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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: INFORMATION: Synthetic construct based on Clostridium botulinum
; OTHER INFORMATION: sequence
; NAME/KEY: CDS
; LOCUS: 10910186a.9 (1159)
US-09-910-186a.9

Alignment Scores:
Score: 4,076-230
Length: 1371
Mismatches: 450
Conservative: 0
Identical: 0
Gaps: 0
Percent Similarity: 100.00%
Percent Identical: 100.00%
Query Match: 34

US-09-910-186a-10 (1-450) X US-09-910-186a-9 (1-1371)
Qy 1 MethThleProHeAnlelPheSerTyThrAnSerLeuLeuAspIlelle 20
Dy 1 ATGACATCACTCAATCAATGTTCTTCTAGCAACACATCTCTTCAGGACATC 59
Qy 21 AenProLlePheAnlelAnSerSerTyLleLeuSerLeuLeuAspIle 40
Dy 20 AACGACTACTTCAACATCAACATCAAGCATCAAGATCTCTCTCTCCAGAACCTAGAAC 29
Qy 41 ThrLeuValPhePheSerGlyTyThrAlaAlaGluValSerGluGluValPheValGluLeu 60
Dy 40 ACCTTGGTGACACCTCCGGTTTACAAGCCGAGGCTCTCCGAGAGAGAGGTCGACACTG 389
Qy 61 AenProLlePheProPheAlaPheValGluLeuSerSerGlyValSerLeuValGlyVal 80
Dy 60 AACCAATCTTCCATATCGACTTCAACCTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
Qy 81 IleValThrGluAlaGluLleValTyThrAnSerMetTyLleGluSerPheSerLleSer 100
Dy 80 CTCTGACACACAGAGAGACATCTCTCTCAACATCCATAGCTACGATCTTCTCTCATCTCC 309
Qy 101 PheTrpLleArgLleAnLeTyTrpValSerAnleuProGlyTyThrLleLeuPheSer 120
Dy 100 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 121 ValGluAnleAnSerGlyTyTrpSerTylleTyLleSerAnPheLeuValPheThrLeu 140
Dy 120 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 141 TygGluAnleAnSerGlyTyTrpSerTylleTyLleSerAnPheLeuValPheThrLeu 160
Dy 140 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 161 ProGlyTyThrAnTyTrpPhePheValThrValThrAnAnSerMetGlyAnleuLeuLys 180
Dy 160 CTCTGATCAACACATGAGTCTCTCTGATCACTCAACATCAACATCAACATCAACATGAG 549
Qy 181 TleGlyTleAlaSerGlyGluAlaSerPheThrLleArgTyLleGluLeuPheThrGlyLleAn 200
Dy 180 ATCTCAACACATGAGTCTCTCTGATCACTCAACATCAACATCAACATCAACATCAACAT 549
Qy 201 PheSerGlyTyLleThrPheAlaLleAlaSerLeuLeuPheThrGluLleThrSer 220
Dy 200 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 221 ApperAnleAnlelAnSerMetTyLlePheValPheValGluLeuAsp 240
Dy 220 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 241 GlytyrAnleAnlelAlaPheAnSerLeuGlyTyThrAnValValGlyAspTy 260
Dy 240 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 261 TrpLleAnlePheArgTyAnleTyGlyTyThrMetValleAnleAspTyThrLeuAn 280
Dy 260 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: INFORMATION: Synthetic construct based on Clostridium botulinum
; OTHER INFORMATION: sequence
; NAME/KEY: CDS
; LOCUS: 10910186a.9 (1159)
US-09-910-186a.9

Alignment Scores:
Score: 4,076-230
Length: 1371
Mismatches: 450
Conservative: 0
Identical: 0
Gaps: 0
Percent Similarity: 100.00%
Percent Identical: 100.00%
Query Match: 34

US-09-910-186a-10 (1-450) X US-09-910-186a-9 (1-1371)
Qy 1 MethThleProHeAnlelPheSerTyThrAnSerLeuLeuAspIlelle 20
Dy 1 ATGACATCACTCAATCAATGTTCTTCTAGCAACACATCTCTTCAGGACATC 59
Qy 21 AenProLlePheAnlelAnSerSerTyLleLeuSerLeuLeuAspIle 40
Dy 20 AACGACTACTTCAACATCAACATCAAGCATCAAGATCTCTCTCTCCAGAACCTAGAAC 29
Qy 41 ThrLeuValPhePheSerGlyTyThrAlaAlaGluValSerGluGluValPheValGluLeu 60
Dy 40 ACCTTGGTGACACCTCCGGTTTACAAGCCGAGGCTCTCCGAGAGAGAGGTCGACACTG 389
Qy 61 AenProLlePheProPheAlaPheValGluLeuSerSerGlyValSerLeuValGlyVal 80
Dy 60 AACCAATCTTCCATATCGACTTCAACCTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
Qy 81 IleValThrGluAlaGluLleValTyThrAnSerMetTyLleGluSerPheSerLleSer 100
Dy 80 CTCTGACACACAGAGAGACATCTCTCTCAACATCCATAGCTACGATCTTCTCTCATCTCC 309
Qy 101 PheTrpLleArgLleAnLeTyTrpValSerAnleuProGlyTyThrLleLeuPheSer 120
Dy 100 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 121 ValGluAnleAnSerGlyTyTrpSerTylleTyLleSerAnPheLeuValPheThrLeu 140
Dy 120 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 141 TygGluAnleAnSerGlyTyTrpSerTylleTyLleSerAnPheLeuValPheThrLeu 160
Dy 140 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 161 ProGlyTyThrAnTyTrpPhePheValThrValThrAnAnSerMetGlyAnleuLeuLys 180
Dy 160 CTCTGATCAACACATGAGTCTCTCTGATCACTCAACATCAACATCAACATCAACATGAG 549
Qy 181 TleGlyTleAlaSerGlyGluAlaSerPheThrLleArgTyLleGluLeuPheThrGlyLleAn 200
Dy 180 ATCTCAACACATGAGTCTCTCTGATCACTCAACATCAACATCAACATCAACATCAACAT 549
Qy 201 PheSerGlyTyLleThrPheAlaLleAlaSerLeuLeuPheThrGluLleThrSer 220
Dy 200 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 221 ApperAnleAnlelAnSerMetTyLlePheValPheValGluLeuAsp 240
Dy 220 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 241 GlytyrAnleAnlelAlaPheAnSerLeuGlyTyThrAnValValGlyAspTy 260
Dy 240 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469
Qy 261 TrpLleAnlePheArgTyAnleTyGlyTyThrMetValleAnleAspTyThrLeuAn 280
Dy 260 TCTTGATCAATCAATCAATCAATGAGTCTCTCAACTTCCGGTTACACATCAATCAATCC 469

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[illegible][illegible]

[illegible]

Query Match: 96.99% Indels: 1
DB: 43 Gaps: 0

US-09-910-186a-10 (1.450) x US-10-271-012-61 (1.502)

QY 4 PropheamrlePheMetTyrrThraAanSerLeuLeuLysAspIleLeuLeuGly 23
DB 152 CCATATGAGGTGGTATGCTATGCTAGTACGCTGTTATTAAGATATTAATATGATA 211
QY 23 PheAanrlePhePhePheSerTyrrIleLysSerLeuLeuLeuLeuLeuLeuLeuLeu 43
DB 23 PheAanrlePhePhePheSerTyrrIleLysSerLeuLeuLeuLeuLeuLeuLeuLeu 43
QY 212 TTTCAATATTTATGATTAATCAAAATTTAGAGCTACAAAGAGAAAGAACTACTTAT 271
DB 43 IAsrThrSerGlyTrpIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 69
QY 272 GATATCATGAGTATATGATGAGATGATGATGAGGAGGATGATGATGATGATGATGAT 331
DB 63 ePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 83
QY 332 ATTTCCATTTGACCTTTATGATTTAGTATGATGATGATGATGATGATGATGATGATGAT 391
DB 103 ektAlaGuanIleValIleValIleValIleValIleValIleValIleValIleVal 391
QY 392 CAG 451
DB 451 TACTTACAGTGTGATATGAGTATATGATATGATATGATATGATATGATATGATATGATAT 511
QY 123 nAnSerGlyTrpSerIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 143
DB 143 TACTTACAGTGTGATATGAGTATATGATATGATATGATATGATATGATATGATATGATAT 571
QY 572 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
DB 163 PheAanrlePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 183
QY 631 CCATTAATATGATTTTGTACTGTTTACATGATATGATGATGATGATGATGATGATGAT 691
DB 203 ektAlaGuanIleValIleValIleValIleValIleValIleValIleValIleVal 203
QY 751 ektAlaGuanIleValIleValIleValIleValIleValIleValIleValIleVal 751
DB 751 ektAlaGuanIleValIleValIleValIleValIleValIleValIleValIleVal 751
QY 203 strIlePheGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 223
DB 223 ACTTATACATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 811
QY 811 CCATTAATATGATTTTGTACTGTTTACATGATATGATGATGATGATGATGATGATGAT 871
DB 871 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
QY 263 pIleAanrlePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 283
DB 283 nAnSerGlyTrpSerIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 331
QY 991 TGATTTTATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 991
DB 303 tyrrAlaAnSerGlyIleValIleValIleValIleValIleValIleValIleValIle 303
QY 1051 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
DB 323 nAnSerGlyTrpSerIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 323
QY 1111 CCATTAATATGATTTTGTACTGTTTACATGATATGATGATGATGATGATGATGAT 1111
DB 343 ektAlaGuanIleValIleValIleValIleValIleValIleValIleValIleVal 343
QY 1171 AGAGATGATTTTATTTTGTATGATGATATGATATGATATGATATGATATGATATGAT 1171

QY 343 sAnslrThrMetTyrrAlaAspAanSerThrGluAspIleTyrrAlaIleGlyLeuLeu 363
DB 1177 GAGTGAACCTATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 1231
QY 363 gdlGlyGlnGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 383
DB 1331 AGCAG 1391
QY 383 tyrrTyrrAlaSerGlnIlePhePhePhePhePhePhePhePhePhePhePhePhe 403
DB 1293 TATATATGATGATATGATATGATATGATATGATATGATATGATATGATATGATAT 1351
QY 403 eysSerIleLeuTyrrGlnPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 423
DB 1411 GGTGCTACTGCTGAGCAGAGAAAGTAATGCTTATGATGATGATGATGATGATGAT 1471
QY 443 gdlGlyPheValProValSerCdu 456

RESULT 15

US-09-611-419A-11
Sequence 11,000,000 Application US/096114.9A
APPLICANT: Smith, Leonard A.
APPLICANT: Byrne, Michael P.
APPLICANT: Klotz, Robert L.
APPLICANT: Klotz, Robert L.
APPLICANT: Clayton, Michael A.
APPLICANT: Brown, Douglas R.
TITLE OF INVENTION: NEUROTOXIN
FILE REFERENCE: A33426 067252.0105
CURRENT FILING DATE: 2000-07-09/611.419A
PRIORITY FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US00/12890
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/133,866
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/133,867
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/133,868
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/133,869
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1999-07-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTA3.0 for Windows Version 4.0
LENGTH: 1374

SYNOPSIS: Artificial Sequence
FEATURES: OTHER INFORMATION: Synthetic construct based on BOMIA 1C
FEATURE: CDL
LOCATION: (10)...(1362)
US-09-611-419A-11

Alignment Scores:
Pred. No.: 7.94e-77 Length: 1374
Score: 886.50 Matches: 187
Best Local Similarity: 43.20% Mismatches: 145
Query Match: 36.32% Indels: 28
Gaps: 11

US-09-910-186A-10 (1-450) X US-09-611-419A-11 (1-1374)


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db 1207 -----CCTTACCAAAAT-----GAGAACGTCCAAAGACTTTGAAGCATTA 128
      355 uspiyrlfaliirlyfeau5glgltwhr----- 366
qy 1351 AGAGCGCTATGGTAGAATTACAGATGATCTGGGCACAGTCMCAATATATTATTA 1310
qy 367 -----Lysapipilaeapapillilepelin 376
      1311 TOTGCCAATCAGATATATTACAACCTGAATTATAGA 1350

RESULT
US-10-240-485-131/c
GENERAL INFORMATION US/10204045
APPLICANT: OLEF, Alexander
APPLICANT: BERNHARDT, Christian
APPLICANT: BERNHARDT, Christian
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APPLICANT: BERLIN, KURT
TITLE OF INVENTION: Diagnosis of Diseases Associated with

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TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.10078, US/10,240,485
PRIORITY NUMBER: US/10,240,485
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10013058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10013773.8
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043262.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 202
SEQ ID NO 131
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SEQ ID NO 133
SEQ ID NO 134
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SEQ ID NO 196
SEQ ID NO 197
SEQ ID NO 198
SEQ ID NO 199
SEQ ID NO 200
SEQ ID NO 201
SEQ ID NO 202
ORGANISM: Artificial Sequence
TYPE: DNA
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US/10-240-485-131

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Alignment Scores:	0.036	6070
Seq. No.:	112.00	113
Length:	112.00	113
Conservative:	35.84	68
Percent Similarity:	22.38	173
Best Local Similarity:	22.38	173
Mismatches:	4.68	153
Every Match:		26
Gaps:		26

2000-05-07 07:45:00 (UTC) 2000-05-07 07:45:00 (UTC)

10 TyrThrAsnAsnSerLeuLeuLysAspIle-----IleAsnGluTyrPheAsn----- 25

3740 TACACGATATA-----CTAATAATCTAATAAATAAATAAATCTCTAATACACATAC 3688

26 -----AgriTelenorSertvatTeletenSertendInbenArq.vgAanTh-Ion 42

[illegible]

DB 3686 ACCCTCCCAAACTAAACCAAAAAAAAAATCAATCCCTA-----AATTAACCTA 363

Qy 43 ValAspThrSerGlyTyrAsnAlaGluValSerGluGluGlyAspValGlnLeuAsnPro 62

3638 ATATGCAATTCTATGATTTATTAACACGCAATTATACCTA---CCACTTAAAAAAGACCA 3598

Year	Number of cases	Percentage of cases
1990	10	0.0001
1991	15	0.0002
1992	20	0.0003
1993	25	0.0004
1994	30	0.0005
1995	35	0.0006
1996	40	0.0007
1997	45	0.0008
1998	50	0.0009
1999	55	0.0010
2000	60	0.0011
2001	65	0.0012
2002	70	0.0013
2003	75	0.0014
2004	80	0.0015
2005	85	0.0016
2006	90	0.0017
2007	95	0.0018
2008	100	0.0019
2009	105	0.0020
2010	110	0.0021
2011	115	0.0022
2012	120	0.0023
2013	125	0.0024
2014	130	0.0025
2015	135	0.0026
2016	140	0.0027
2017	145	0.0028
2018	150	0.0029
2019	155	0.0030
2020	160	0.0031
2021	165	0.0032
2022	170	0.0033
2023	175	0.0034
2024	180	0.0035
2025	185	0.0036
2026	190	0.0037
2027	195	0.0038
2028	200	0.0039
2029	205	0.0040
2030	210	0.0041
2031	215	0.0042
2032	220	0.0043
2033	225	0.0044
2034	230	0.0045
2035	235	0.0046
2036	240	0.0047
2037	245	0.0048
2038	250	0.0049
2039	255	0.0050
2040	260	0.0051
2041	265	0.0052
2042	270	0.0053
2043	275	0.0054
2044	280	0.0055
2045	285	0.0056
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2056	340	0.0067
2057	345	0.0068
2058	350	0.0069
2059	355	0.0070
2060	360	0.0071
2061	365	0.0072
2062	370	0.0073
2063	375	0.0074
2064	380	0.0075
2065	385	0.0076
2066	390	0.0077
2067	395	0.0078
2068	400	0.0079
2069	405	0.0080
2070	410	0.0081
2071	415	0.0082
2072	420	0.0083
2073	425	0.0084
2074	430	0.0085
2075	435	0.0086
2076	440	0.0087
2077	445	0.0088
2078	450	0.0089
2079	455	0.0090
2080	460	0.0091
2081	465	0.0092
2082	470	0.0093
2083	475	0.0094
2084	480	0.0095
2085	485	0.0096
2086	490	0.0097
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2088	500	0.0099
2089	505	0.0100
2090	510	0.0101
2091	515	0.0102
2092	520	0.0103
2093	525	0.0104
2094	530	0.0105
2095	535	0.0106
2096	540	0.0107

63ilepheprophe 66
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Db 3581 AAACCAATATATTCACACACCAATTCCTACCAAAATACAAAAATCTAATACCATC 3582

67 AspPheIValLeuGlySerSerGlyGluAspArgGlyValg-----79

[illegible]

DB 3521 CTCTAGACATTCCAAGGAAATAGAAAAAANANUNCCTCCCTCAGTCAATTTCATAA 349

Qy 80 -----ValIleValThrGlnAngLysAsnIleValTyrAsnSerMetTyrGlu 95

22-23
 24-25
 26-27
 28-29
 30-31
 32-33
 34-35
 36-37
 38-39
 40-41
 42-43
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6291 CACTACATATACGCGAAC-----ATAACACTCAATAT 6256
 173 Aenlenmeteslyanmetysille-Tyrileanoglylsaulleapthreily 192
 6295 AACACATTAATACATACAAAAATATATACACAGCAGCATATACACTACTA 6196
 192 svalysaglyluThuglylelanPheselysthelethPhedjulle----- 209
 6195 AAAAAACACCTCATCATATACAAATATATACCTCGATCCCTAAAA 6136
 209 ----- 209
 6135 AACTATCATACACACACATCCACACACACACACACACACACAAATTAACCT 6076
 210 -----AsulyalleToAsPheslyleulle----- 218
 6075 ACACACACATTAATACAAAAAATACATCCCTCTTCCTCTCTATATATAC 6016
 219 -----ThSeApSeApAsnIleAsnMetIpIear 230
 6015 CAAACCTTACCTTCGCTACCTCACACTCTCTTCAATCACTTAACTC----- 5964
 230 gspPhyTyleAlalygluleanoglylsAsplean---IleleuPhas 249
 5963 AACCTTCCTTCACANCTTCGAAACACCTCCCTCTATATACACATATTCAC 5905
 249 0-----8e 250
 5904 ATACTCATATATTACCTCAATATTTAAACGACACTAAACACATTTTA 5845
 250 flegdlyThAsnVallylsasphyTtpolyAsnAspIau----- 265
 5844 TTAAATTTCAATTCCTTCAAAATTAATTCCTTTTAACACTATATATATAT 5785
 266 -AspTyAsnLygluTyTymetVelanIleasPhyTyleanAsnGlyTymety-A 285
 5844 CCAATATCTCCCATAC-----TTAAACAACATTTTAAAT-----CACCC 5740
 285 laAsSerAsgInIleAlaPhasThAsgAsyAsnAsnAspPhasAspPhasgIuglyT 305
 5739 CTACACTACTCAATCAACACACACAAATTAATCATCAATATATAATCTACCT 5680
 305 yrlvs---IleIleIlelyAsgIleAsgIyAnThAsnAspThAsyAlAsgIy 324
 5679 ATAACTTATTTCTATCCCTTTTCCTTCCTTAAATCATCTATT----- 5627
 324 lyAspIleAsuTyPhasPhetThIlelanAsnlyAlatyAsnleuPhaslelysa 344
 5626 -----CCTCTTTTATCTCA-----ANCTCATATCTTAAATCAATATACCTAAAA 5575
 344 sgluthmetTyAlaAsnHISerThgluAspIetyAlaIleIlelyleuArg 364
 5574 ARNAAAGCG-----TCANCTTTCCTCTCAATTAATTCCTTTCCTTACATAC- 5522
 364 lugIleThlyAspIleAsnAsnIleIlePhedIleIlePromet----- 380
 5521 -----TCCAAARAAATCTCAACAAATATCAAAATATATATACAT 5479
 381 -----AsrAsnThTyTyrAlaSerGlnIlePhesAsnPhasg 397
 5478 AACTATCAGCATAT-----TATTTCGACAAATTAATAAACATTAATA 5425
 397 IyGluAn 399
 5424 TTTCAAT 5417

Search completed: November 7, 2002, 20:05:40
 Job time : 62 sec

Genome version 5.1.3
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OK protein - protein search, using aa model
(without alignments)
1005,038 Million cell updates/sec

Run on: November 7, 2002, 14:41:56, Search time 43 seconds

Title: US09-910-186a-10
Score: 35.09
Sequence: 1 MTFPFIKSYFVNSLKEII.....NVASLSESTHGKPPVSE 450

Scoring table: BLSDSW62
Gap 10.0, Gapext 0.5

Marched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 04
Maximum Match 1048
Creating first 49 summaries

Database: 1: Pir31:
2: Pir2:
3: Pir3:
4: Pir4:

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2386	95.8	1291	2	846431	botulinum neurotoxin
2	2386	95.8	1291	2	A49777	botulinum neurotoxin
3	1823	78.2	1395	2	S70582	botulinum neurotoxin
4	1823	78.2	1395	2	S81957	botulinum neurotoxin
5	801.5	31.0	1207	2	S81957	botulinum neurotoxin
6	594.5	25.9	1252	2	S21178	botulinum neurotoxin
7	594	24.8	1251	2	JM0256	botulinum neurotoxin
8	585.9	24.5	1256	1	BTCLAR	botulinum neurotoxin
9	585.9	24.5	1256	1	BTCLAR	botulinum neurotoxin
10	581	24.3	1291	1	A48940	botulinum neurotoxin
11	565.9	23.8	1259	2	S40515	botulinum neurotoxin
12	565.9	23.8	1259	2	S40515	botulinum neurotoxin
13	549.5	23.0	1374	2	J40813	botulinum neurotoxin
14	382.5	17.8	1315	1	BTCLIN	botulinum neurotoxin
15	382.5	17.8	1315	1	BTCLIN	botulinum neurotoxin
16	379	11.7	366	2	S48110	botulinum neurotoxin
17	245.5	10.3	369	2	S48109	botulinum neurotoxin
18	230.5	9.6	1162	2	A49879	botulinum neurotoxin
19	230.5	9.6	1162	2	A49879	botulinum neurotoxin
20	213	8.9	1193	2	S68218	botulinum neurotoxin
21	199	8.3	1165	2	J40644	botulinum neurotoxin
22	199	8.3	1165	2	J40644	botulinum neurotoxin
23	199	8.3	1196	2	S46430	botulinum neurotoxin
24	191.5	8.0	1193	2	JC4901	botulinum neurotoxin
25	171.5	7.3	960	2	S72284	botulinum neurotoxin
26	171.5	7.3	960	2	S72284	botulinum neurotoxin
27	170.5	7.1	398	1	S39V41	botulinum neurotoxin
28	168.5	7.0	1817	2	474611	botulinum neurotoxin
29	168	7.0	4688	2	F82865	botulinum neurotoxin

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ALIGNMENTS

RESULT 1

S46431
N:Human neurotoxin C1 - Clostridium botulinum phage IC (strain C 468)
N:Alternate name: RoNT/C1 protein
C:Species: Clostridium botulinum phage IC
A:Variety: strain C 468
C:Accession: S46431; S49107
R:Hauser, D.; Eklund, M.W.; Boquet, F.; Popoff, M.R.
A:Title: Organization of the botulinum neurotoxin C1 gene and its associated non-toxic A subunit
A:Accession: S46431; S49107
A:Molecule type: DNA
A:Residues: 1-1991 <RAW>
A:Residues: 1-1991 <RAW>
A:Experimental source: strain C 468
A:Note: the nucleotide sequence was submitted to the EMBL data Library, May 1993
C:Superfamily: tetanus toxin

Query Match

Query Match	Similarity	100.0%	99.8%	Score	2386	DB	2	Length	1291
Matches	44%	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Q1	2	TIPFSTTNELLGDIINETPNRISGILSIQRNKTIVTDSYVSEEDVQLN	61						
DB	843	TIPFSTTNELLGDIINETPNRISGILSIQRNKTIVTDSYVSEEDVQLN	902						
Q2	63	PITFPGKSSGSGRGVTVQNTENVNMTSFISPIFNINRWVSLPGTILISV	121						
DB	903	PITFPGKSSGSGRGVTVQNTENVNMTSFISPIFNINRWVSLPGTILISV	962						
Q3	128	KNGSGSGLISFVPLTQNLSESSVNSFQISNASKVNSVFNWVNSGNGKNT	181						
DB	963	KNGSGSGLISFVPLTQNLSESSVNSFQISNASKVNSVFNWVNSGNGKNT	1022						
Q4	183	YVNGKIDITKVEGFGNSKFTFPIVPIQGITSDQNTNMTVFYFAKELG	341						
DB	1022	YVNGKIDITKVEGFGNSKFTFPIVPIQGITSDQNTNMTVFYFAKELG	1082						
Q5	242	KDILNFSGLQTVNKKVGNGLVWYKTYVQVYINRWVANSQIVNFSNNDF	301						
DB	1082	KDILNFSGLQTVNKKVGNGLVWYKTYVQVYINRWVANSQIVNFSNNDF	1142						
Q6	302	MGKTKIKRNTQNGNVAGDGLVPDMTNNAKLPKMKETAKNHSSTEDYVIG	361						
DB	1142	MGKTKIKRNTQNGNVAGDGLVPDMTNNAKLPKMKETAKNHSSTEDYVIG	1202						
Q7	362	MEQTVQDINKIPQIQPMNTVYASQIFKNSFNSGTSIGISITAFPLGQWRIN	421						
DB	1202	MEQTVQDINKIPQIQPMNTVYASQIFKNSFNSGTSIGISITAFPLGQWRIN	1262						

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Search completed: November 7, 2002, 14:45:49
Job time : 53 secs

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binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The c-terminus of the heavy chain (4) is responsible for the binding of the light chain (5) to the vesicle membrane and mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (1) blocking neurotransmitter release. Mutation of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure. **CLINICAL ACTIVITY:** Limited hydrolysis of proteins of the neuromuscular apparatus: synaptobrevins, SNAP25 or syntaxin. No detectable action on small molecule substrates. **GENE:** CHAT. **HEAVY CHAIN (4):** Middle-linked heterodimer of a light chain (1) and a heavy chain (4). **CELLULAR LOCATION:** Secreted. **POST-TRANSLATIONAL MODIFICATION:** N-linked glycosylation. **FUNCTION:** Available under the pseudonym of choline acetyltransferase, this enzyme is involved in the synthesis of acetylcholine and in the regulation of synaptic transmission and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders. **DEFECT:** Defect in the CHAT gene causes the autosomal recessive disorder CHAT deficiency. **DISORDERS:** There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G. **CAUTION:** Botulinum neurotoxin is a potent neurotoxin. **SEQUENCE DATA:** NEMO-TOX product information Web site: www.bottox.com/index.jsp#productinfo. **WWW-TOX:** Nemo-protein spotlight: www.bottox.com/index.jsp#protein.

WWW="http://www.expiry.org/spotlight/articles/april0319.html".

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Search completed: November 7, 2002, 14:44:02
 Job time : 34 secs

Copied from 10910186 on 05-05-2004

~~Copied from 10910186 on 05-05-2004~~

Qy 389 Q-IPKSNFNSGSGICGTYIFRFG-----DNYRHTVPLVQGNAS 434
 Db 1222 QLFKFK--DESDTDLGIGIHNFYSGVYKVFCLSNWY----LAKVAKPTNS 1274
 Qy 435 LLRSTSHWYFVPSR 450
 Db 1275 KL---GCMQGFIPKDE 1287
 RESULT 8
 Q9AZA18 Q9AZA18 PRELIMINARY; PRT: 1291 AA.
 AC Q9AZA18
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
 DE Type B botulinum toxin.
 DE BONT.
 DE Clostridium botulinum.
 DE Clostridia; Bacillus/Clostridium group; Clostridia;
 DE Clostridiales; Clostridiaceae; Clostridium.
 DE NCBI_Taxid:1491.
 DE SOURCE FROM N.A.
 DE STRAIN=CDC 3241.
 DE SWISSPROT=84021; Emboss:Q97710.
 DE CHARACTERIZATION OF THE GENES ENCODING THE BOTULINUM NEUROTOXIN
 DE IN A COMPLEX IN A STRAIN OF CLOSTRIDIUM BOTULINUM PRODUCING TYPE B & F
 DE Curr_Microbiol. 37:317-318(1998).
 EMBL: Y11630; CA73968.1; -
 DR P11630; F11630; F11630.
 DR HSPCS:227.002.
 DR InterPro: IPR000395; Bontotoxilin.
 DR InterPro: IPR000130; Zn_MTPetpde.
 DR InterPro: IPR000130; Zn_MTPetpde.
 DR PRINTS: PR00760; BONTOMILYSIN 1.
 DR PRODOM: PD001963; Bontotoxilin; 1.
 DR PROSITE: PS00147; ZINC METALLOPROTEIN; UNKNOWN 1.
 DR SEQUENCE 1291 AA, 110840 MW, 24250PM, 163273 CS CRC64:
 Query Match 25.3%, Score 604, 7 pa 2, Length 1291.
 Mismatches 167; Conservative 81; Mismatches 135; Indels 90; Gaps 20;
 2 TIFPNTSYNLSADLIDNYRNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 61
 835 SIPDLSITNTLITLFIYNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 894
 63 PIFPPEKSGEDGVQNTYNTYNSVSTGNSVANSYEDGVQNL 115
 895 D---KAGLTSSA--NSKLVGNQNTLINSNLDVSVNPIKPKQDQNTIHRY 930
 115 TIDVNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 174
 951 THICKNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 1010
 175 MGNKVIYINKLIDTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----WIR 230
 1011--SKMVIYINKLIDTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GRNDQVQINK 1057
 2031--SKMVIYINKLIDTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 1093
 236 AKGLDQNTLNSQGLTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 1093
 1058 VTSIFVLSLSNLTUETKLSKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLK 1117
 287 SQVETPNNRNN-----DNEYVYLIKIKRNN---NOTVAGEDLIVDFDINK 336
 2113 VGLTSLNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 1176
 337 ATKVFNKNTYADNDSTETALGLAKK---DINDNIF---OTQPMNTYIAS 386
 1177 ENRYVY-----YTKFKKELFAPISDSDEFNTQIKRDEPTTSS 1221

Qy 389 Q-IPKSNFNSGSGICGTYIFRFG-----DNYRHTVPLVQGNAS 434
 Db 1222 QLFKFK--DESDTDLGIGIHNFYSGVYKVFCLSNWY----LAKVAKPTNS 1274
 Qy 435 LLRSTSHWYFVPSR 450
 Db 1275 KL---GCMQGFIPKDE 1287
 RESULT 9
 Q9FAM06 Q9FAM06 PRELIMINARY; PRT: 1255 AA.
 AC Q9FAM06
 DT 01-MAY-2001 (TrEMBLrel. 16, Created)
 DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
 DE Type B botulinum toxin.
 DE CN.
 DE Clostridium botulinum.
 DE Clostridia; Bacillus/Clostridium group; Clostridia;
 DE Clostridiales; Clostridiaceae; Clostridium.
 DE NCBI_Taxid:1491.
 DE SOURCE FROM N.A.
 DE STRAIN=CDC 3241.
 DE SWISSPROT=84021; Emboss:Q97710.
 DE CHARACTERIZATION OF THE GENES ENCODING THE BOTULINUM NEUROTOXIN
 DE IN A COMPLEX IN A STRAIN OF CLOSTRIDIUM BOTULINUM PRODUCING TYPE B & F
 DE Curr_Microbiol. 37:317-318(1998).
 EMBL: Y11630; CA73968.1; -
 DR P11630; F11630; F11630.
 DR HSPCS:227.002.
 DR InterPro: IPR000395; Bontotoxilin.
 DR InterPro: IPR000130; Zn_MTPetpde.
 DR InterPro: IPR000130; Zn_MTPetpde.
 DR PRINTS: PR00760; BONTOMILYSIN 1.
 DR PRODOM: PD001963; Bontotoxilin; 1.
 DR PROSITE: PS00147; ZINC METALLOPROTEIN; UNKNOWN 1.
 DR SEQUENCE 1255 AA, 113916 MW, 185578986, 163273 CS CRC64:
 Query Match 25.2%, Score 602.5, 6 pa 2, Length 1255.
 Mismatches 167; Conservative 81; Mismatches 134; Indels 69; Gaps 18;
 2 TIFPNTSYNLSADLIDNYRNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 61
 825 SIPDLSITNTLITLFIYNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 884
 62 PIFPPEKSGEDGVQNTYNTYNSVSTGNSVANSYEDGVQNL 117
 885 TIFPNT--GIYNDKLSVNTLVKVELGNGSKTFEINPKIDGLTSSNSIN 942
 943--KNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 175
 943--KNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 1002
 176 MGNKVIYINKLIDTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 235
 1003--SKMVIYINKLIDTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 1093
 236 AKGLDQNTLNSQGLTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 1093
 1054 QRLDQNTLNSQGLTIVKVELGNGSKTFEINPKIDGLTSSNSIN-----GLTFNIF 1111
 292 ENRYVY-----DNEYVYLIKIKRNN---NOTVAGEDLIVDFDINK 347
 1112 VNTSLNSNSKSLDKRNLKLVSTGNSVANSYEDGVQNL 1165
 348 TADNHSSTETALGLAKK---DINDNIF---OTQPMNTYIAS 395
 1166 YATATYVY-----KNTKLTSSNSNSNSNSNSNSNSNSNSNSNSNSNSNS 1211

[illegible]

NCBI-TxId=1449:
1 SOURCE FROM N.A.
2 STRAIN=KELDND 178 ATCC52455;
3 MEDLINE=9412659; PubMed=7764370;
4 Huxton R.A., Collins M.D., East A.K., Thompson D.E.: Polyvinyl
5 chloride binds to the extracellular domain of the neurotoxin,
6 clostridial neurotoxin₁.
7 Curr. Microbiol. 28:101-110(1994).
8 !- FUNCTION: BOWLING GREEN TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
9 RELEASE FROM PRESYNAPTIC TERMINALS AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL
10 CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS.
11 INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
12 BINDING SITE.
13 !- IDENTIFICATION: HEAVY CHAIN (H). THE HEAVY CHAIN HAS THE PHARMACOLOGICAL ACTIVITY
14 OF BOTULINUM NEUROTOXIN TYPE A.
15 WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN FORM A LIGHT CHAIN (L) AND AN
16 UNUSUAL DISULFIDE-BINDING SITE.
17 !- FORMATION AND TOXIN FINDING, RESPECTIVELY.
18 !- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
19 BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

[illegible][illegible]

HB3 isolate cultured *in vitro*, was digested with mung bean nuclease in the presence of 30% formaldehyde at 50°C (Vernick et al., 1986). The reaction mixture was extracted with phenol, and the DNA fraction was precipitated by ethanol. The DNA was purified by repeated extractions with chloroform and water, and then resuspended in distilled water. The ends of the fragments were polished using T4 DNA polymerase, and the fragments were ligated to EcoR V-cleaved and dephosphorylated E. coli vector pUC19. Recombinant plasmids transformed E.

COLL ADJ-BIG.			
BASE COUNT	286 a	45 c	68 g
	175 t	1 others	

Alignment Scores:	
Prod. No.:	0.000455
Score:	17.00
Percent Similarity:	36.73%
Best Local Similarity:	25.00%
Query Match:	4.89%
DB:	17
Length:	575
Matches:	49
Conservative:	23
Mismatches:	75
Indels:	48
Gaps:	6

$$100 - 0.0001968 \times 10^4 (1.450) \times 2540915 (-575)$$

[illegible]

10910 F86 on 05-05-2004

10910186 2005-05-2004

Copied from 10910186 on 05-05-2004

Best Local Similarity	43.64;	Prod. No. 7.7e-20;	
Matches	483;	Conservative	0; Mismatches 490; Indels 0; gaps 0;
QY	237	CAGAGTAAAGTCTGATGATCCACACAGAGAGATGCTGTCTACATCCATGACATGATC	295
DQ	2947	CAC	98581
DQ	337	CT	335
DQ	98680	TAC	98621
QY	357	CATCATGATCTCTGTCAC	416
DQ	98520	CAC	98551
DQ	98560	CAC	98501
DQ	477	CTCCAC	536
DQ	98500	CAC	98441
QY	537	GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	536
DQ	98440	CAC	98381
DQ	98400	CAC	98351
DQ	98380	CAC	98321
DQ	557	TCGTAC	716
DQ	98320	CAC	98251
DQ	717	CAGAGTAAAGTCTGATGATCCACACAGAGAGATGCTGTCTACATCCATGACATG	776
DQ	98260	CAC	98201
DQ	777	CTGAC	836
DQ	98200	CAC	98141
DQ	837	CTGCT	896
DQ	98140	CAC	98081
DQ	987	TAC	956
DQ	98080	CAC	98021
DQ	957	CAC	1016
DQ	98020	CAC	97961
DQ	1017	GCT	1076
DQ	97960	CAC	97901
QY	1077	CATCTAGACATCTGCTGTGAC	1136
DQ	97900	CAC	97841
DQ	1137	GATCCAC	1196
DQ	97840	CAC	97781
QY	1197	CGTGTGATGATC	1209
DQ	97780	CAC	97768

RESULT 11

AC117007/c	176331 bp	DNA	linear	HTO 17-JUL-2002
LOCUS	176331 bp	DNA	linear	HTO 17-JUL-2002
DEFINITION	176331 bp	DNA	linear	HTO 17-JUL-2002
ACCESSION	176331 bp	DNA	linear	HTO 17-JUL-2002
VERSION	176331 bp	DNA	linear	HTO 17-JUL-2002
KEYWORDS	176331 bp	DNA	linear	HTO 17-JUL-2002
SOURCE	176331 bp	DNA	linear	HTO 17-JUL-2002
ORGANISM	176331 bp	DNA	linear	HTO 17-JUL-2002
REFERENCE	176331 bp	DNA	linear	HTO 17-JUL-2002
AUTHORS	176331 bp	DNA	linear	HTO 17-JUL-2002
TITLE	176331 bp	DNA	linear	HTO 17-JUL-2002
ABSTRACT	176331 bp	DNA	linear	HTO 17-JUL-2002
KEYWORDS	176331 bp	DNA	linear	HTO 17-JUL-2002
COMMENT	176331 bp	DNA	linear	HTO 17-JUL-2002

Scanned with CamScanner

[illegible]

[illegible][illegible]

REFERENCE

1 (bases 1 to 169163)

AUTHORS

Murzy, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratinge, H.C., Are, J.R., Ayete, M., Banks, T., Barbara, T., Benton, Y., Birnagol, V., Blakemore, V., Boal, D., Rattus.

Search completed: November 7, 2002, 13:24:47
 Elapsed time : 3520 secs

GenScore version 5.1.3
Copyright (c) 1993 - 2002 CompuLink Ltd.

DN nucleic - nucleic search, using av model

Run on: November 7, 2002, 11:02:35 ; search time 253 seconds

File: US-09-910-186a-9
(without alignments)
Sequence: 12579-13171 Willcox cell updates/sec

Score: 1544226.0
Sequence: 1544226.0
Gap: 10.0, Gapset 1.0

Scoring table: F80V7K WUC

Gap: 10.0, Gapset 1.0

Number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Minimum DB seq length: 0

Post-processing: Minimum Match 0%

Listing first 45 summaries

Base :

1: Genes: 101302+ :

2: /SID52/gcdgata/geneseq-emb1/NA1380.DAT *

3: /SID52/gcdgata/geneseq-emb1/NA1381.DAT *

4: /SID52/gcdgata/geneseq-emb1/NA1382.DAT *

5: /SID52/gcdgata/geneseq-emb1/NA1383.DAT *

6: /SID52/gcdgata/geneseq-emb1/NA1384.DAT *

7: /SID52/gcdgata/geneseq-emb1/NA1385.DAT *

8: /SID52/gcdgata/geneseq-emb1/NA1386.DAT *

9: /SID52/gcdgata/geneseq-emb1/NA1387.DAT *

10: /SID52/gcdgata/geneseq-emb1/NA1388.DAT *

11: /SID52/gcdgata/geneseq-emb1/NA1389.DAT *

12: /SID52/gcdgata/geneseq-emb1/NA1390.DAT *

13: /SID52/gcdgata/geneseq-emb1/NA1391.DAT *

14: /SID52/gcdgata/geneseq-emb1/NA1392.DAT *

15: /SID52/gcdgata/geneseq-emb1/NA1393.DAT *

16: /SID52/gcdgata/geneseq-emb1/NA1394.DAT *

17: /SID52/gcdgata/geneseq-emb1/NA1395.DAT *

18: /SID52/gcdgata/geneseq-emb1/NA1396.DAT *

19: /SID52/gcdgata/geneseq-emb1/NA1397.DAT *

20: /SID52/gcdgata/geneseq-emb1/NA1398.DAT *

21: /SID52/gcdgata/geneseq-emb1/NA1399.DAT *

22: /SID52/gcdgata/geneseq-emb1/NA1400.DAT *

23: /SID52/gcdgata/geneseq-emb1/NA1401.DAT *

24: /SID52/gcdgata/geneseq-emb1/NA1402.DAT *

25: /SID52/gcdgata/geneseq-emb1/NA1403.DAT *

26: /SID52/gcdgata/geneseq-emb1/NA1404.DAT *

27: /SID52/gcdgata/geneseq-emb1/NA1405.DAT *

28: /SID52/gcdgata/geneseq-emb1/NA1406.DAT *

29: /SID52/gcdgata/geneseq-emb1/NA1407.DAT *

30: /SID52/gcdgata/geneseq-emb1/NA1408.DAT *

31: /SID52/gcdgata/geneseq-emb1/NA1409.DAT *

32: /SID52/gcdgata/geneseq-emb1/NA1410.DAT *

33: /SID52/gcdgata/geneseq-emb1/NA1411.DAT *

34: /SID52/gcdgata/geneseq-emb1/NA1412.DAT *

35: /SID52/gcdgata/geneseq-emb1/NA1413.DAT *

10 199.8 14.6 1317 22 AA54490 Botulin toxin hsa
11 198.2 14.5 1317 21 AA87216 DNA encoding synth
12 198.2 14.5 1317 21 AA87216 DNA encoding synth
13 169.4 12.4 1324 22 AA54485 Botulin toxin hsa
14 169.4 12.4 1402 17 AA23246 Type A neurotoxin
15 169.4 12.4 1402 17 AA23246 Clostridium botuli
16 169.4 12.4 1402 17 AA23246 Clostridium botuli
17 168.8 12.3 1330 17 AA23245 Type A neurotoxin
18 168.8 12.3 1330 19 AA230571 Clostridium botuli
19 168.8 12.3 1330 19 AA230571 Clostridium botuli
20 168.8 12.3 1330 19 AA230571 Clostridium botuli
21 162.4 11.8 1400 21 AA87215 DNA encoding synth
22 162.4 11.8 1400 21 AA87215 DNA encoding synth
23 162.4 11.8 1400 21 AA87215 DNA encoding synth
24 151.8 11.1 1314 22 AA54499 Botulin toxin hsa
25 151.8 11.1 1314 22 AA54499 Botulin toxin hsa
26 151.8 11.1 1314 22 AA54499 Botulin toxin hsa
27 147.2 10.7 985 24 AB544817 Oligonucleotide co
28 145.8 10.6 1332 22 AA54488 Sequence encoding
29 136 9.9 5163 21 AA20700 Cyprosporidium pa
30 136 9.9 5163 21 AA20700 Cyprosporidium pa
31 136 9.9 5163 21 AA504778 C parvum gp900 gen
32 136 9.9 5318 21 AA61948 DNA encoding a por
33 136 9.9 5318 21 AA61948 DNA encoding a por
34 134 9.8 5318 19 AA20701 Cyprosporidium
35 133.6 9.7 7417 23 AB16968 Brosephilia melano
36 126.6 9.2 102 23 AA87221 DNA encoding BONF
37 126.6 9.2 102 23 AA87221 DNA encoding BONF
38 121 8.8 2607 23 AB16369 Brosephilia melano
39 120.4 8.8 1341 21 AA87213 DNA encoding synth
40 119.4 8.8 1341 21 AA87213 DNA encoding synth
41 115 8.4 5511 21 AA61947 Botulin toxin hsa
42 115 8.4 5511 21 AA61947 Botulin toxin hsa
43 115 8.4 5511 21 AA61947 Botulin toxin hsa
44 115 8.4 7334 21 AA61946 Cyprosporidium pa
45 110.6 8.1 3597 23 AA53137 DNA encoding novel

ALIGNMENTS

RESULT 1
ID AA57214 standard; DNA, 1371 BP.
XX AT
XX AA57214
XX 08-MAY-2000 (first entry)
XX DNA encoding synthetic BONT serotype C (BONT) HC fragment.
XX Botulinum neurotoxin, heavy chain, BONT; serotype C.
XX C-terminal fragment; Venezuelan equine encephalitis virus replicon.
XX VBS; botulinum; vaccine; diagnosis; drug screening; ds.
XX Clostridium botulinum.
XX Synthetic.
XX Key
XX CDS
XX Isolation/Qualifiers
XX 101362
XX /Product= "Synthetic botulinum neurotoxin serotype C
(BONT); heavy chain C-terminal fragment (hc)"
XX W020000224.A2.
XX 20-JAN-2000.
XX 09-JUL-1999; 99NO-US15570
XX 10-JUL-1998; 98US-0092416
XX 12-MAY-1999; 99US-013870.
XX

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	ID	Description
1	1371	100.0	1371	22	AA54490
2	1371	100.0	1371	22	AA54490
3	665.2	48.5	3950	20	AA23246
4	645.8	46.4	1502	19	AA23058
5	526.4	38.4	1440	21	AA23631
6	526.4	38.4	1440	21	AA23631
7	420.2	30.6	1374	22	AA54487
8	420.2	30.6	1374	22	AA54487
9	217.4	15.9	1368	22	AA54491

Query Match 38.4% Score 526.4; DB 21; Length 1440;
Best local Similarity 65.9%;
Matches 799; Conservative 0; Mismatches 401; Indels 12; Gaps

[illegible]


```

Query Match      12.4%  Score 159.4, DB 19, Length 1402;
Seq. Locs. Similarity 34.4%  P-Val No. 2e-27;
Matches 456; Conservative 6; Mismatches 341; Indels 42; Gaps 4;

OY 41 CGACACACTCCGCTGTGAGGAGACATCATGACGAGTACTCTGACAGATCATGACGACTCA 100
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 68 CTAGCATGGCTGTGCTGTCTGCTTACCTTCTGATGATGATGATGATGATGATGATGAT 127
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 101 AGATCTGTGCTGTGAGACGCTGAGACGCTGAGACGCTGAGACGCTGAGACGCTGAGAC 160
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 128 CACTCTGTGACCTGCTGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 187
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 161 AGTGTGCGAGAGAGGAGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 220
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 188 AATTCACCTGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 246
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 221 GTTCTCTCGGTGAGAGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 280
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 247 -----TGTATCTGTGATCTTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCT 301
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 281 ACTCATGTGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 302 ACTCATGTGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 341 ACTTGC-----AGGTACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 362 CCATCTCTCTGAGACATGATACCATCATCATCATCATCATCATCATCATCATCATCATCAT 421
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 392 CCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 422 AAGTATCTGGAATCTGAGTGAATCATCTGAGACTCTGAGAGACTCTGAGAGAAATCAAC 481
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 482 ATTCATCACTGCTGCTGAGCACTCTGCAACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 508
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 482 AGCGTGTGTATCTCAATATCTCTGAGTGTGATGATGATGATGATGATGATGATGATGAT 541
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 509 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 542 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 569 TGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 602 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 629 TCGAGTACAGAGATCCGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 688
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 642 TCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 697
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 689 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 698 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 757
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 749 TGTTCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 758 TGTACGACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 817
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 809 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 818 AGGCAACACCTACTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 876
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: November 7, 2002, 12:25:57
 Job time : 264 secs

NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: OPND-01763
TELEPHONE: (415) 705-8410
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 base pairs
STRANDNESS: double
TOPOLOGY: linear
MOLWEIGHT TYPE: DNA (genomic)
NAME/FEATURE: CDS
FEATURES: 1..1386
US-08-405-436a-25

Query Match 12.44; Score 169.4; DB 1: Length 1402;

Best Local Similarity 54.4%; Gaps 42; Indels 42; Gaps 4;

Matches 456; Conservative 0; Mismatches 341; Indels 42; Gaps 4;

41. CCMACACCTCCCTGTGAAGAGATCACTGACGAGTCTTCACACATGACGATCCCA 100

68 CTACACAGCTCGCTGCTGCTACTCTGCTACCTGCTACATGACACACATGATCACT 127

101 AACTGCTGCTGCTGCGACACCGGTAGACAGCTGTGGGACACCTGGGTAGACAGCG 160

128 CACTGCTGACCTGGCTGACACATGACATGATGATGATGATGATGATGATGATGAT 187

161 AGGCTGTCGACAGAGGCTGAAGCTGACGATGACACCTGCTGCTGCTGCTGCTGCT 220

188 AATTCACATGCTGCTTGAAGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246

221 GTTCTCGCTGAGGACGAGGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280

247 ----TTCAATCTGGAAATCTTCACATGACGATGCTGCTGCTGCTGCTGCTGCTGCT 301

281 ACTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

302 ACTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

341 ACTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391

362 CACTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421

392 CACTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451

421 AGATGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481

452 ATGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508

481 ATGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541

509 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568

541 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

569 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 628

601 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

628 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688

661 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725

688 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748

725 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787

748 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 808

787 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847

808 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867

847 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907

867 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927

907 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967

927 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987

967 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000

987 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060

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1120 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240

1180 TGTGCTGCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1300

DB 818 AGACACACCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 876

RESULT 2

US-08-405-436a-25

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

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Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a

Sequence 25 Application US/08405436a


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QY 737 ACATCAATCTGTTGAACTCTTGATGATACACACAGCTGTCAGGAGTACTGGGTA 796
DB 1111111111111111111111111111111111111111111111111111111
QY 3076 TCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3135
DB 1111111111111111111111111111111111111111111111111111111
QY 797 AGCACTGATACACACACACACACACACACACACACACACACACACACACACAC 856
DB 1111111111111111111111111111111111111111111111111111111
QY 3136 ATACTACTAGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3189
DB 1111111111111111111111111111111111111111111111111111111
QY 857 TGTAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
DB 1111111111111111111111111111111111111111111111111111111
QY 3190 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3249
DB 1111111111111111111111111111111111111111111111111111111
QY 917 AGCTGATACACACACACACACACACACACACACACACACACACACACACAC 976
DB 1111111111111111111111111111111111111111111111111111111
QY 3250 TGCATGATACACACACACACACACACACACACACACACACACACACACAC 3309
DB 1111111111111111111111111111111111111111111111111111111
QY 977 TGTGCTGATACACACACACACACACACACACACACACACACACACACACAC 1036
DB 1111111111111111111111111111111111111111111111111111111
QY 3310 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3369
DB 1111111111111111111111111111111111111111111111111111111
QY 1037 AGACACACACACACACACACACACACACACACACACACACACACACAC 1096
DB 1111111111111111111111111111111111111111111111111111111
QY 3370 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3429
DB 1111111111111111111111111111111111111111111111111111111
QY 1097 TGTGACACACACACACACACACACACACACACACACACACACACACAC 1156
DB 1111111111111111111111111111111111111111111111111111111
QY 3430 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1489
DB 1111111111111111111111111111111111111111111111111111111
QY 1157 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216
DB 1111111111111111111111111111111111111111111111111111111
QY 3490 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3549
DB 1111111111111111111111111111111111111111111111111111111
QY 1217 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
DB 1111111111111111111111111111111111111111111111111111111
QY 3550 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3596
DB 1111111111111111111111111111111111111111111111111111111

```

RESULT 14

Sequence 13

us-08-471-033-18

Application US/08/471033

GENERAL INFORMATION

APPLICANT: Warren, Gregory W

APPLICANT: Kozlowski, Michael G

APPLICANT: Kozlowski, Michael A

APPLICANT: Nye, Gordon

APPLICANT: Carl, Brian

APPLICANT: Kozlowski, Michael

APPLICANT: Kozlowski, Michael

APPLICANT: Duck, Nicholas B

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

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APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

APPLICANT: Ertuch, Juan J

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: APPLICATION NUMBER: US 08/218,018
: FILING DATE: 23-MAR-1994
: PRIOR APPLICATION DATA: US 08/037,057
: PUBLICATION NUMBER: US 08/037,057
: FILING DATE: 25-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: P-40,403
: REFERENCE/DOCKET NUMBER: CQC 1695/C193/DIV7 - SQUW3
: TELECOMMUNICATIONS INFORMATION:
: TELEPHONE: 919-541-8692
: TELEFAX: 919-541-8693
: INFORMATION FOR SEQ ID NO. 18:
: SEQUENCE LENGTH: 3004
: SEQUENCE DESCRIPTION:
: LENGTH: 3004 base pairs
: TYPE: nucleic acid
: TOPOL: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOHETICAL: NO
: FEATURE: NO
: NAME/KEY: misc_feature
: ORIGIN: 1
: OTHER INFORMATION:
: /note= "wise optimised DNA
: sequence for VIF(A) 80 kd protein from A878"
: US-08-471-033-18

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Query Match      6.88; Score 93.4; DB 3; Length 2004;
Best Local Similarity 44.38; Pred. No. 6.10e-12;
Matches 539; Conservative 0; Mismatches 631; Indels 15; Gaps 3;
QY 51 CCGTGTGAAGGAGCATCATCAAGAGTACTGACGACATCAACATCAAGATCTGTC 110
DB 1111111111111111111111111111111111111111111111111111111
QY 378 CGGAGGCGGCGCATCGCTCCCGAGGCGGATCACTTCGGCTGAGCTGATCTACGCA 437
DB 1111111111111111111111111111111111111111111111111111111
QY 438 CAGCGAGCTGCTGCGGCGGAGTGGGCGACGACGACGACGACGACGACGACGAC 497
DB 1111111111111111111111111111111111111111111111111111111
QY 171 GAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227
DB 1111111111111111111111111111111111111111111111111111111
QY 498 CGGCGCGCGCTACCTGACGACGACGACGACGACGACGACGACGACGACGACGAC 557
DB 1111111111111111111111111111111111111111111111111111111
QY 228 GCGTGAAGCAGAGTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
DB 1111111111111111111111111111111111111111111111111111111
QY 558 CTGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 617
DB 1111111111111111111111111111111111111111111111111111111
QY 678 CTGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 737
DB 1111111111111111111111111111111111111111111111111111111
QY 618 CGCGAGTGAAGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 677
DB 1111111111111111111111111111111111111111111111111111111
QY 348 AGTTCACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 407
DB 1111111111111111111111111111111111111111111111111111111
QY 678 CGMAGCGGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 737
DB 1111111111111111111111111111111111111111111111111111111
QY 408 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 467
DB 1111111111111111111111111111111111111111111111111111111
QY 738 CAGAGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
DB 1111111111111111111111111111111111111111111111111111111
QY 468 CTGAGCATCTCAGACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
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QY 798 CGMAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
DB 1111111111111111111111111111111111111111111111111111111
QY 528 CAGAGCTGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 584
DB 1111111111111111111111111111111111111111111111111111111
QY 858 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
DB 1111111111111111111111111111111111111111111111111111111
QY 585 ---GCTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641
DB 1111111111111111111111111111111111111111111111111111111
QY 918 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 977
DB 1111111111111111111111111111111111111111111111111111111
QY 642 GATCCGAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
DB 1111111111111111111111111111111111111111111111111111111

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[illegible]

SOURCE: APPLE MACINTOSH MICROSOFT ACQU 0.0
 SEQ ID NO 3
 LENGTH: 1317
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: /note="synthetic sequence encoding botulinum neurotoxin"
 05-1-2008-09:350-751-5

Query Match	Similarity	Score	198.2	DB 10	Length	1317			
Matches	436	Conservative	0	Mismatches	333	Indels	48	Gaps	5
QY	27	CACCTCTGCTGCTGACACACCTCTCTGTTGACGACGACACACGACGACGACGACCA	85						
DB	6	CAGAGTGTCTCTACACGACGACGATCTGATCTGTCTCTACAGCTGTCTCTACGAA	55						
QY	87	CATCAGCATCTCAGATCTCTCTGCTGACAGCATGTAAGACATCTGTGCGACGCTC	146						
DB	65	GATCAGACGACCTCTCTCTTGACATGACATGACGACGACGACGACGACGACGACG	125						
QY	141	GGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	206						
DB	126	GGTTGCTGGTCTGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	185						
QY	207	GCACTCTAAGCTGGGTCTCTCCGGTGGAGGACAGAGTCACTGCTCAACGACGACA	266						
DB	185	CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	239						

[illegible]

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Query Match      12.8%; Score 168.8; DB 10; Length 1338;
Best Local Similarity 54.8%; Pred. No. 5.6e-33;
Matches 447; Conservative 0; Mismatches 331; Indels 42; Gaps
4;
Dy 64 ATCTATGAGGAGTCTTCAACATGAGAGAGAGTCAAGATGAGTCTGCTCTGAGAGAGCT 123
Dy 27 ATCTATGAGGAGTCTTCAACATGAGAGAGAGTCAAGATGAGTCTGCTCTGAGAGAGCT 86
Dy 124 AGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 183
Dy 87 TCAATGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGT 146
Dy 188 CAGTCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGT 243
Dy 147 ACTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGT 200
Dy 244 AGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 303
Dy 207 AATGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 260
Dy 304 AATGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 354
Dy 261 ACTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGT 320
Dy 325 ACAGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 414
Dy 321 ACAGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 380
Dy 415 CTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 474
Dy 381 ATGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 440
Dy 475 ATCTCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGT 531
Dy 441 CAGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 500
Dy 532 ATGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 591
Dy 501 CTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 560
Dy 592 GAGTCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 631
Dy 561 AATCTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 620
Dy 653 ACAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 711
Dy 621 ATCTGAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 656
Dy 712 TCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 771
Dy 715 TCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 716
Dy 831 ACAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 831
Dy 777 GAGTCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 776
Dy 832 AGATGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 867
Dy 777 ATCTCAAGAGAGTCTGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCTGAGAGAGAGTCT 812

RESULT 6
: Sequence 4, Application US/9350756
: Patent No. US20020034521A1
: APPLICANT: US: Army Medical Research Institute for Infectious Diseases
: APPLICANT: John S. Lee
: APPLICANT: Peter Furbush
: APPLICANT: Peter Furbush
: APPLICANT: Jonathan F. Smith
: APPLICANT: Mark T. Dertzbaugh
: APPLICANT: Leonard Smith

```

1

; TYPE: DNA

~~Copied from 10910186 on 05-05-2004~~

```

; ORGANISM: Clostridium botulinum
; FILE REFERENCE: 009124/SNP_R10_98-21
; CURRENT FILING DATE: 1998-07-09
; ORGANISM: Artificial
; OTHER INFORMATION: /note="synthetic sequence encoding botulinum neurotoxin"
US-09-350-756-2

Query Match      9.84; Score 126 61; DB 10; Length 702;
Match Local Similarity 50.74; Pred No. 6.9e+21;
Matches 412; Conservative 0; Mismatches 269; Indels 42; Gaps 3;

; EARLIER APPLICATION NUMBER: US 60/092,416
; INVENTOR: J. S. Smith, et al.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 1: 1
; SEQ ID NO 2: 1
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: /note="synthetic sequence encoding botulinum neurotoxin"
US-09-350-756-2

; 64 ATATCATACAGGATGATTCATCAACATATCAAGCAGCTTCCTCTCGAGACAGCT 123
; 124 AATGACATGCTGGTGGACATCGCTGGTATCAAGCGGAGCTCGGAGGAGAGCTC 183
; 70 GACATCAATCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
; 184 CAGCTGACACCATCTTCCCATCGAGCTTCAGCTGAGCTGCTGCTGCTGCTGCTGCT 243
; 130 GACATCAATCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 177
; 244 AAGTATCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
; 178 AGATTCGCTGTTATCTGAGATCAATCATCATCATCATCATCATCATCATCATCAT 237
; 304 ATCTCTCTCTGATCATATCAACAAGT- - - - -GCTCTCAACTG 345
; 316 CCGGTGACAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 405
; 298 AATGATACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 357
; 406 TCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
; 358 GTTACAGCTATCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
; 466 TCTTAGAGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
; 418 GATCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 477
; 516 AACAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 585
; 478 ACATCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 537
; 586 GTTACAGGATGCTGAGCTATCAAGCTCTTCCAGAGACATCATCATCATCATCATCAT 645
; 538 ATCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 597
; 646 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
; 598 ATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 633
; 706 TACTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
; 634 TCCATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
; 766 TACATCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 825
; 694 TATCTGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 753
; 826 ATCTGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 887
; 754 AAGTTCATGCTGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903

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US-09-216-393-340
 ; Sequence 340: Application US/09216393
 ; Applicant: Milbausen, Michael James
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
 ; FILE REFERENCE: TX-1-C2
 ; CURRENT APPLICATION NUMBER: US/09/216,393
 ; EARLIER APPLICATION NUMBER: 08/994,925
 ; EARLIER FILING DATE: 1997-12-19
 ; INVENTOR: Milbausen, Michael James
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 340
 ; LENGTH: 867
 ; ORGANISM: Toxoplasma gondii
 ; FEATURE: CDS
 ; LOCATION: 31...1867;
 ; US-09-216-393-340

Query Match
 Best Local Similarity 51.1%; Prod. No. 2e-13; Indels 0; Gaps 0;
 Matches 212; Conservative 0; Mismatches 203;
 QY 734 AGGACATCAACATCTGTTAACTCTCTTCAGTACACCAAGGTGTCAGAGACTACG 793
 DB 451 APTTCATCCAGTAGAGTAGACAGACAGACATCATACCTACTACCTACCTACC 510
 QY 794 GTACGACCTGAGATACACAGACAGACATCATACCTACTACCTACCTACCTAC 853
 DB 511 ACCACTAGACTACTACTACACTAGACACACCACTACACACACACACACT 570
 QY 854 ACGTGTACGACCTGACAGACAGACATCATACCTACTACCTACTACCTACTAC 913
 DB 571 AC 630
 QY 914 AGAGGTGTACAGATCATCATACAGGTATACAGGTATACAGGTATACAGGTATAC 973
 DB 631 AC 690
 QY 974 GAGGTGTACAGATCATCATACAGGTATACAGGTATACAGGTATACAGGTATAC 1033
 DB 1034 TTAGAGACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATACAG 1093
 QY 1094 TCGGTGTACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATAC 1148
 DB 811 ACTACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATACAGGTAT 865

RESULT 15
 US-09-216-393-342
 ; Sequence 342: Application US/09216393
 ; Applicant: Milbausen, Michael James
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
 ; FILE REFERENCE: TX-1-C2
 ; CURRENT APPLICATION NUMBER: US/09/216,393
 ; EARLIER APPLICATION NUMBER: 08/994,925
 ; EARLIER FILING DATE: 1997-12-19
 ; INVENTOR: Milbausen, Michael James
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 342
 ; LENGTH: 867

; TYPE: DNA
 ; ORGANISM: Toxoplasma gondii
 ; US-09-216-393-342
 ; Feature: CDS
 ; Location: 31...1867;
 ; US-09-216-393-342
 Query Match
 Best Local Similarity 51.1%; Prod. No. 2e-13; Indels 0; Gaps 0;
 Matches 212; Conservative 0; Mismatches 203;
 QY 734 AGGACATCAACATCTGTTAACTCTCTTCAGTACACCAAGGTGTCAGAGACTACG 793
 DB 451 APTTCATCCAGTAGAGTAGACAGACAGACATCATACCTACTACCTACCTACC 510
 QY 794 GTACGACCTGAGATACACAGACAGACATCATACCTACTACCTACCTACCTAC 853
 DB 511 ACCACTAGACTACTACTACACTAGACACACCACTACACACACACACACT 570
 QY 854 ACGTGTACGACCTGACAGACAGACATCATACCTACTACCTACTACCTACTAC 913
 DB 571 AC 630
 QY 914 AGAGGTGTACAGATCATCATACAGGTATACAGGTATACAGGTATACAGGTATAC 973
 DB 631 AC 690
 QY 974 GAGGTGTACAGATCATCATACAGGTATACAGGTATACAGGTATACAGGTATAC 1033
 DB 1034 TTAGAGACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATACAG 1093
 QY 1094 TCGGTGTACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATAC 1148
 DB 811 ACTACAGAGGTGTACAGGTATACAGGTATACAGGTATACAGGTATACAGGTAT 865

Search completed: November 7, 2002, 14:41:50
 Job time : 68 secs

GenCore version 5.1.3

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ON nucleic - nucleic search, using sw model

Run on: November 7, 2002, 12:21:30 Search time 3155 seconds

US-09-910-186a-9
1371
Sequence: 1 gatttcagctgactacc.....tcttcagtaataaggaaattc 1371

Scoring table: IDENTITY MKC

Gapop 10.0 Gapop 1.0

24791104 seeds, 1571243825 residues 49882208

Minimal DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database: Pending cypates NA-Melo:*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

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2	1371	99.6	1371	17	US-09-910-186a-9
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Sequence 9, Application US/99910186A
GENERAL INFORMATION: Medical Research & Material Command
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTOR: NEUROTOXIN
CURRENT APPLICATION NUMBER: US/99/05/10186A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/99/05/10186A
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 09/613,665
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,666
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,667
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,668
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,669
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,673
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 09/613,675
PRIOR FILING DATE: 1993-09-21
SUBJECT OF SEQ ID NOS: 34
SOURCE: GenBank
SEQ ID NO 9: Feature for Windows Version 4.0

LENGTH: 1371
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
NAME/KEY: CDS
LOCATION: (21)...(1375)
US-09-910-186a-9

Query Match
Match: 100.0% Score: 1371; DB: 34; Length: 1371;
Match: 100.0% Similarity: 100.0% Pos: 3, 58-79;
Match: 1371; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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RESULT 3

US-09-350-756-3
 Sequence 3 Application US/0930756
 APPLICANT: John S. Lee
 APPLICANT: U.S. Army Medical Research Institute for Infectious Diseases
 APPLICANT: Michael D. Parker
 APPLICANT: Mark E. Dierckx
 APPLICANT: Jonathan F. Smith
 APPLICANT: Mark E. Dierckx
 TITLE OF INVENTION: Botulinum Neurotoxin Vaccine
 FILE REFERENCE: 003/124/SAP R1D 98-31
 CURRENT FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: US 60/092,416
 NUMBER OF SEQ. ID NOS.: 198-07-10
 SOFTWARE: Apple Macintosh Microsoft Word 6.0
 SEQ. ID NO. 3, 171
 TYPE: DNA
 ORGANISM: Artificial
 OTHER INFORMATION: /note="synthetic sequence encoding botulinum neurotoxin"

US-09-350-756-3
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 Best Local Similarity 99.8%; Pred. No. 3,96-278;
 Matches 168; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Scanned with 10910186 on 05-05-2004

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RESULT 4

US-09-15394-59
 Sequence 59 Application PC/708715394
 GENERAL INFORMATION:
 APPLICANT: Thayer, Bruce S.
 TITLE OF INVENTION: Multivalent Vaccine For Clostridium
 TITLE OF INVENTION: Botulinum Neurotoxin

LOCATION: (1), (3876)

FUNCTION INFORMATION:

AUTHORS: Baudouin

TITLE: Organization of the botulinum neurotoxin C1 gene and

TITLE: its associated non-toxic protein genes in Clostridium

JOURNAL: Mol. Gen. Genet.

VOLUME: 243

PAGES: 631-640

DATABASE ACCESSION NUMBER: GeneBank / X72793

DATABASE ENTRY DATE: 1993-05-03

MIM NUMBER: 120386

US-10-205-53-5

Query Match 48.54, Score 655.2, Gap 42, Length 3876,
 Best Local Similarity 58.34, Best Match 7e-138,
 Matches 922, Conservative 0, Mismatches 428, Indels 0, Gaps 0;
 13 ACACGCCATCAACATCTCTGATCAACAGCACTCGCTGTGACAGCACTGATCAAC 72
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 73 GAGTACTCAACATCACTCAACATCTCAACATCTGCTGCTGACGATCAACATCAAC 132
 2587 GAAATATTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2646
 133 TTGCTGACACCTCCGCTGACACCGGAGCTGCTCGAGAGAGGCTGCTCGACGTGAC 192
 2647 TTGCTGACACCTCCGCTGACACCGGAGCTGCTCGAGAGAGGCTGCTCGACGTGAC 2706
 193 CCAATCTCCCATCTGACATCAAGCTGGGCTCTCCGCTGGAGAGAGGTAAGTCACT 282
 2707 CCAATCTCCCATCTGACATCAAGCTGGGCTCTCCGCTGGAGAGAGGTAAGTCACT 2766
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 3067 TATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3216
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RESUME 7

US-00-271-012-59

Sequence 59, Application: US/10271012

GENERAL INFORMATION: Invs. James A.

APPLICANT: Thalley, Bruce S.

TITLE OF INVENTION: Multivalent Vaccine for Clostridium

NUMBER OF SEQUENCES: 1, Multinomial Neurotoxin

CORRESPONDENCE ADDRESS:

ADDRESS: Medline & Carroll

CITY: San Francisco

STATE: California

COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/271,012

FILING DATE: 15-Oct-2002

CLASSIFICATION: <div>A01N 63/00

APPLICATION NUMBER: US/08/704,159

FILING DATE: <div>A01N 63/00

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: 0PHD-02304

TELEPHONE: (415) 705-8410

Oy 133 TTGTCGACACTCGCTTACACGCGAGCTCCGAGAGAGTGAAGTCCAGCTGAC 192
 Db 2659 TAGTGAGTACACAGATATATACAGAGAGAGTGAAGAGAGAGTTCAGCTATAT 2718
 Oy 193 CCATCT 252
 Oy 2719 CCATATCT 2778
 Db 253 CTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 312
 Db 2779 GTTACGAGATAGATATATATATATATATATATATATATATATATATATAT 2839
 Oy 313 TGATGACGATACACAGAGGAGGACGACGACGACGACGACGACGACGACGACG 372
 Db 2859 TGATGACGATACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 498
 Oy 373 AGGACACT 432
 Db 2895 AAGATACACT 2958
 Oy 432 CAGACGAGGACGACGAGGACGACGACGACGACGACGACGACGACGACGACG 492
 Db 2959 GATATAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3018
 Oy 492 GTTACGAGATAGATATATATATATATATATATATATATATATATATATAT 552
 Db 3019 GATATAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3078
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Oy 1213 GTTATCTGCTCCACTGCTACCTACGATCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
 Db 3739 GATATAGAT 3798
 Oy 1273 TACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
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RESULT 10
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 Sequence 4, Application US/09710237
 Applicant: Walker, Patricia
 Title of Invention: Methods of Treating Hyperhidrosis
 Current Application Number: US/09/730,237
 Current Filing Date: 2000-12-05
 Number of SEQ ID NOS: 12
 SEQ ID NO 4 Patent Ver. 2.1
 Length: 3876
 Organism: Botulinum toxin
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 Db 2527 ACATACCT 2586
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 DB 3307 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3366
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and is derived by analysis of the total score distribution.

SUMMARIES

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2 50 2 3028 5 US-09-448-939A-218 Sequence 218, Ap
3 42 3 3028 5 US-09-448-939A-218 Sequence 218, Ap
4 50 6 3 3561 6 US-10-092-411A-1685 Sequence 1685, Ap
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8 47 6 3 3561 6 US-10-092-411A-1685 Sequence 1685, Ap
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: Sequence 1585: Application US/1024425
: GENERAL INFORMATION: Anasadi
: APPLICANT: Boland, Joseph F.
: APPLICANT: Lord, Reginald V.
: APPLICANT: Kewer, Chris
: APPLICANT: Kewer, Chris
: APPLICANT: Scherf, Uwe C.
: APPLICANT: Vorkley, Joseph G.
: FILE REFERENCE: 4493-5026
: CURRENT APPLICATION NUMBER: US/10240425
: PRIORITY APPLICATION NUMBER: US/02019512
: PRIOR FILING DATE: 2001-03-28
: PRIOR APPLICATION NUMBER: US 60/193,446
: NUMBER OF SEQ ID NOS: 588
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NOS: 135259
: TYPE: DNA
: ORGANISM: Homo sapiens
: OTHER INFORMATION: Genbank Accession No. 283838
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Matches 391; Conservative 0; Mismatches 440; Indels 12; Gaps 2;
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: 65406 CATCTACATCATCTGTGTATCATCACTACACATCCATCCATCCATCATCTAC 69465
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